



## SEQUENCE LISTING

### (1) GENERAL INFORMATION:

- (i) APPLICANT: BIOGEN, INC.
- (ii) TITLE OF INVENTION: Ret Ligand (RetL) for Stimulating Neural and Renal Growth
- (iii) NUMBER OF SEQUENCES: 21
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Biogen, Inc.
  - (B) STREET: 14 Cambridge Center
  - (C) CITY: Cambridge
  - (D) STATE: MA
  - (E) COUNTRY: USA
  - (F) ZIP: 02142
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE: 07-MAY-1997
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/999,999
  - (B) FILING DATE: 01-JAN-1996
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Levine, Leslie M.
  - (B) REGISTRATION NUMBER: 35,245
  - (C) REFERENCE/DOCKET NUMBER: A008 PCT CIP
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 617-679-2400
  - (B) TELEFAX: 617-679-2838

### (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3616 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 257..1660

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

60 GCGGCCGCAG GTTGGGTCGG AACTGAACCC CTGAAAGCGG GTCCGCCTCC CGCCCTCGCG  
120 CCCGCCCGGA TCTGAGTCGC TGGCGGCGGT GGGCGGCAGA GCGACGGGGA GTCTGCTCTC  
180 ACCCTGGATG GAGCTGAACT TTGAGTGGCC AGAGGAGCGC AGTCGCCCCG GGATCGCTGC  
240 ACGCTGAGCT CTCTCCCCGA GACCGGGCGG CGGCTTTGGA TTTTGGGGGG GCGGGGACCA  
289 GCTGCGCGGC GGCACC ATG TTC CTA GCC ACT CTG TAC TTC GCG CTG CCA  
Met Phe Leu Ala Thr Leu Tyr Phe Ala Leu Pro  
1 5 10  
337 CTC CTG GAT TTG CTG ATG TCC GCC GAG GTG AGT GGT GGA GAC CGT CTG  
Leu Leu Asp Leu Leu Met Ser Ala Glu Val Ser Gly Gly Asp Arg Leu  
15 20 25  
385 GAC TGT GTG AAA GCC AGC GAT CAG TGC CTG AAG GAA CAG AGC TGC AGC  
Asp Cys Val Lys Ala Ser Asp Gln Cys Leu Lys Glu Gln Ser Cys Ser  
30 35 40  
433 ACC AAG TAC CGC ACA CTA AGG CAG TGC GTG GCG GGC AAG GAA ACC AAC  
Thr Lys Tyr Arg Thr Leu Arg Gln Cys Val Ala Gly Lys Glu Thr Asn  
45 50 55  
481 TTC AGC CTG ACA TCC GGC CTT GAG GCC AAG GAT GAG TGC CGT AGC GCC  
Phe Ser Leu Thr Ser Gly Leu Glu Ala Lys Asp Glu Cys Arg Ser Ala  
60 65 70 75  
529 ATG GAG GCC TTG AAG CAG AAG TCT CTG TAC AAC TGC CGC TGC AAG CGG  
Met Glu Ala Leu Lys Gln Lys Ser Leu Tyr Asn Cys Arg Cys Lys Arg  
80 85 90  
577 GGC ATG AAG AAA GAG AAG AAT TGT CTG CGT ATC TAC TGG AGC ATG TAC  
Gly Met Lys Lys Glu Lys Asn Cys Leu Arg Ile Tyr Trp Ser Met Tyr  
95 100 105  
625 CAG AGC CTG CAG GGA AAT GAC CTC CTG GAA GAT TCC CCG TAT GAG CCG  
Gln Ser Leu Gln Gly Asn Asp Leu Leu Glu Asp Ser Pro Tyr Glu Pro  
110 115 120  
673 GTT AAC AGC AGG TTG TCA GAT ATA TTC CGG GCA GTC CCG TTC ATA TCA  
Val Asn Ser Arg Leu Ser Asp Ile Phe Arg Ala Val Pro Phe Ile Ser  
125 130 135  
721 GAT GTT TTC CAG CAA GTG GAA CAC ATT TCC AAA GGG AAC AAC TGC CTG  
Asp Val Phe Gln Gln Val Glu His Ile Ser Lys Gly Asn Asn Cys Leu  
140 145 150 155

769 GAC GCA GCC AAG GCC TGC AAC CTG GAC GAC ACC TGT AAG AAG TAC AGG  
 Asp Ala Ala Lys Ala Cys Asn Leu Asp Asp Thr Cys Lys Lys Tyr Arg  
 160 165 170

817 TCG GCC TAC ATC ACC CCC TGC ACC ACC AGC ATG TCC AAC GAG GTC TGC  
 Ser Ala Tyr Ile Thr Pro Cys Thr Thr Ser Met Ser Asn Glu Val Cys  
 175 180 185

865 AAC CGC CGT AAG TGC CAC AAG GCC CTC AGG CAG TTC TTC GAC AAG GTT  
 Asn Arg Arg Lys Cys His Lys Ala Leu Arg Gln Phe Phe Asp Lys Val  
 190 195 200

913 CCG GCC AAG CAC AGC TAC GGG ATG CTC TTC TGC TCC TGC CGG GAC ATC  
 Pro Ala Lys His Ser Tyr Gly Met Leu Phe Cys Ser Cys Arg Asp Ile  
 205 210 215

961 GCC TGC ACC GAG CGG CGG CGA CAG ACT ATC GTC CCC GTG TGC TCC TAT  
 Ala Cys Thr Glu Arg Arg Arg Gln Thr Ile Val Pro Val Cys Ser Tyr  
 220 225 230 235

1009 GAA GAA CGA GAG AGG CCC AAC TGC CTG AGT CTG CAA GAC TCC TGC AAG  
 Glu Glu Arg Glu Arg Pro Asn Cys Leu Ser Leu Gln Asp Ser Cys Lys  
 240 245 250

1057 ACC AAT TAC ATC TGC AGA TCT CGC CTT GCA GAT TTT TTT ACC AAC TGC  
 Thr Asn Tyr Ile Cys Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys  
 255 260 265

1105 CAG CCA GAG TCA AGG TCT GTC AGC AAC TGT CTT AAG GAG AAC TAC GCA  
 Gln Pro Glu Ser Arg Ser Val Ser Asn Cys Leu Lys Glu Asn Tyr Ala  
 270 275 280

1153 GAC TGC CTC CTG GCC TAC TCG GGA CTG ATT GGC ACA GTC ATG ACT CCC  
 Asp Cys Leu Leu Ala Tyr Ser Gly Leu Ile Gly Thr Val Met Thr Pro  
 285 290 295

1201 AAC TAC GTA GAC TCC AGC AGC CTC AGC GTG GCA CCA TGG TGT GAC TGC  
 Asn Tyr Val Asp Ser Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys  
 300 305 310 315

1249 AGC AAC AGC GGC AAT GAC CTG GAA GAC TGC TTG AAA TTT CTG AAT TTT  
 Ser Asn Ser Gly Asn Asp Leu Glu Asp Cys Leu Lys Phe Leu Asn Phe  
 320 325 330

1297 TTT AAG GAC AAT ACT TGT CTC AAA AAT GCA ATT CAA GCC TTT GGC AAT  
 Phe Lys Asp Asn Thr Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn  
 335 340 345

1345 GGC TCA GAT GTG ACC ATG TGG CAG CCA GCC CCT CCA GTC CAG ACC ACC  
 Gly Ser Asp Val Thr Met Trp Gln Pro Ala Pro Pro Val Gln Thr Thr  
 350 355 360

1393 ACT GCC ACC ACT ACC ACT GCC TTC CGG GTC AAG AAC AAG CCT CTG GGG  
 Thr Ala Thr Thr Thr Thr Ala Phe Arg Val Lys Asn Lys Pro Leu Gly  
 365 370 375

1441 CCA GCA GGG TCT GAG AAT GAG ATC CCC ACA CAC GTT TTA CCA CCC TGT  
 Pro Ala Gly Ser Glu Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys  
 380 385 390 395

1489 GCG AAT TTG CAG GCT CAG AAG CTG AAA TCC AAT GTG TCG GGT AGC ACA  
 Ala Asn Leu Gln Ala Gln Lys Leu Lys Ser Asn Val Ser Gly Ser Thr  
 400 405 410

1537 CAC CTC TGT CTT TCT GAT AGT GAT TTC GGA AAG GAT GGT CTC GCT GGT  
 His Leu Cys Leu Ser Asp Ser Asp Phe Gly Lys Asp Gly Leu Ala Gly  
 415 420 425

1585 GCC TCC AGC CAC ATA ACC ACA AAA TCA ATG GCT GCT CCT CCC AGC TGC  
 Ala Ser Ser His Ile Thr Thr Lys Ser Met Ala Ala Pro Pro Ser Cys  
 430 435 440

1633 AGT CTG AGC TCA CTG CCG GTG CTG ATG CTC ACC GCC CTT GCT GCC CTG  
 Ser Leu Ser Ser Leu Pro Val Leu Met Leu Thr Ala Leu Ala Ala Leu  
 445 450 455

1680 TTA TCT GTA TCG TTG GCA GAA ACG TCG TAGCTGCATC CGGGAAAACA  
 Leu Ser Val Ser Leu Ala Glu Thr Ser  
 460 465

1740 GTATGAAAAG ACAAAGAGA ACCAAGTATT CTGTCCCTGT CCTCTTGAT ATCTGAAAAT

1800 CCAGTTTAA AAGCTCCGTT GAGAAGCAGT TTCACCCAAC TGGAACCTT TCCTTGTTTT

1860 TAAGAAAGCT TGTGGCCCTC AGGGGCTTCT GTTGAAGAAC TGCTACAGGG CTAATTCCAA

1920 ACCCATAAGG CTCTGGGGCG TGGTGCGGCT TAAGGGGACC ATTTGCACCA TGTAAGCAA

1980 GCTGGGCTTA TCATGTGTTT GATGGTGAGG ATGGTAGTGG TGATGATGAT GGTAATTTTA

2040 ACAGCTTGAA CCCTGTTCTC TCTACTGGTT AGGAACAGGA GATACTATTG ATAAAGATTC

2100 TTCCATGTCT TACTCAGCAG CATTGCCTTC TGAAGACAGG CCCGCAGCCT AGTGTGAATG

2160 ACAAGTGGAG GTTGGCCTCA AGAGTGGACT TGGCAGACTC TACCTTGATG TAATGTTTAC

2220 CTTTCCGTGT ATGGTCTCCA CAGAGTGTTT ATGTATTTAC AGACTGTTCT GTGATCCCCC

2280 AACAACAACA ACCACAAATT CCTTGGTCAC CTCCAAATGT AACCGGTCCT TTAGCCCAGT

2340 AGAGGAGGGT GGGTGTGGCC CTGGCACAGC TCCCGGATTG TTGATGGGCA CTCTCCTGAG  
 2400 CTTTGCTTGA GTGAGAAGCT GAATGTAGCT GAAAATCAAC TCTTCTTACA CTTCTTACTG  
 2460 CTTTCGTTTAC TTACGAGGTC ACATATAGAA CAAACATCAC CAACTATTAG CTTACCGTTA  
 2520 GCTTCCCAAC TATTAGCTTT CTATGTTTTG AAAGCAGTGT TGCTGACCCC ATGTTTTAAT  
 2580 GATGGTTTAA TACATGCAGC CCTTTCCTCT CATCGGTAAC ACTAGCTCCA ACATCAACTT  
 2640 CATGCATGTG GCTCTCAAAA GCAGGCCCCA AGAAGCCCAG TTCTTTAGGA GAAAGCTGCG  
 2700 TCCTGTTTCT GTGGACAGGC AGGAGGAAAC AGAGCAGCCT GCCCGTGGTG TCTTTATCTG  
 2760 TTTTGAAATC AAGGCTGCCT GTGTGTAAGG AATGGTTCAA TTCTTATAAA GGGTGCCACT  
 2820 GTTGATGCCA CAACTGGCAG TTGGTCTAGC TCCAGGACAC CGGTTTCCAT GTTGCTGGC  
 2880 AGAGACAGCT TTGATTGGGA CTGGCTGGCC ACAAGGGATG GGATGAAGAT GTGCTGCCCT  
 2940 CTCTTTCAAA GTTGAGCCCT GCCAGGGCAC ATAGAAGCAT CTTTGCTCCT GACCACAACG  
 3000 TAGAACAGCT TGGATTCAAG GTCATCAAGC GTCTCCTGTA CATTGCTCTG TGACCTTCAT  
 3060 AACAGACTGT CCCGCACAAA AGGAACGGCA GTTTATGGAT CTAGAGTGGG AGCACAGGGT  
 3120 CTGGAAAGGT GAACCGATTG GCAAAATACA CAGAACAGGA GGGAGAGTCT CAAGCCGAGA  
 3180 CATCTTGCTT ACTAGCCACA CACCATCTCC TGGAGCCCTC TCCTGACCT GGGCAGACCC  
 3240 TTAGGTGTAT ATCTAAAGAC CTCTTCAATG TTCAGGTTC AATCTGTAA ATGGTTGCGT  
 3300 CCTGGCACCC ATTCTGAAA ACTGAACAAA GGAGAGGATA TCTTTCCTCC ATTGAGCCCT  
 3360 GAAAGTATGA CTGGCTTCTC ACCCTCCAC AGAGCAGGGA GCCCTGGTGC ACACAGTCTC  
 3420 CTGATATCCT CCCTGCTCTT TGAGGTTTGC CTTGGGAGAA AATGATTAC CTCGGGAGGG  
 3480 GACGCTTTGG TGTCTGAAGT ACGTTTATAT CGAAATGTTA ATGAATACCC ATGTAAAATA  
 3540 CTCAATAGCC ACCTTCTTC CCTTCACAAT GTTTTCGAGG GGAATGCATC CAACATCCAA  
 3600 GTGTACCTGG TCAGTGGGAA GTTCCATGAA GACTCATACA TTGAATAAAC ATATTGATG

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 468 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Phe	Leu	Ala	Thr	Leu	Tyr	Phe	Ala	Leu	Pro	Leu	Leu	Asp	Leu	Leu	1	5	10	15
Met	Ser	Ala	Glu	Val	Ser	Gly	Gly	Asp	Arg	Leu	Asp	Cys	Val	Lys	Ala	20	25	30	
Ser	Asp	Gln	Cys	Leu	Lys	Glu	Gln	Ser	Cys	Ser	Thr	Lys	Tyr	Arg	Thr	35	40	45	
Leu	Arg	Gln	Cys	Val	Ala	Gly	Lys	Glu	Thr	Asn	Phe	Ser	Leu	Thr	Ser	50	55	60	
Gly	Leu	Glu	Ala	Lys	Asp	Glu	Cys	Arg	Ser	Ala	Met	Glu	Ala	Leu	Lys	65	70	75	80
Gln	Lys	Ser	Leu	Tyr	Asn	Cys	Arg	Cys	Lys	Arg	Gly	Met	Lys	Lys	Glu	85	90	95	
Lys	Asn	Cys	Leu	Arg	Ile	Tyr	Trp	Ser	Met	Tyr	Gln	Ser	Leu	Gln	Gly	100	105	110	
Asn	Asp	Leu	Leu	Glu	Asp	Ser	Pro	Tyr	Glu	Pro	Val	Asn	Ser	Arg	Leu	115	120	125	
Ser	Asp	Ile	Phe	Arg	Ala	Val	Pro	Phe	Ile	Ser	Asp	Val	Phe	Gln	Gln	130	135	140	
Val	Glu	His	Ile	Ser	Lys	Gly	Asn	Asn	Cys	Leu	Asp	Ala	Ala	Lys	Ala	145	150	155	160
Cys	Asn	Leu	Asp	Asp	Thr	Cys	Lys	Lys	Tyr	Arg	Ser	Ala	Tyr	Ile	Thr	165	170	175	
Pro	Cys	Thr	Thr	Ser	Met	Ser	Asn	Glu	Val	Cys	Asn	Arg	Arg	Lys	Cys	180	185	190	
His	Lys	Ala	Leu	Arg	Gln	Phe	Phe	Asp	Lys	Val	Pro	Ala	Lys	His	Ser	195	200	205	
Tyr	Gly	Met	Leu	Phe	Cys	Ser	Cys	Arg	Asp	Ile	Ala	Cys	Thr	Glu	Arg	210	215	220	
Arg	Arg	Gln	Thr	Ile	Val	Pro	Val	Cys	Ser	Tyr	Glu	Glu	Arg	Glu	Arg	225	230	235	240
Pro	Asn	Cys	Leu	Ser	Leu	Gln	Asp	Ser	Cys	Lys	Thr	Asn	Tyr	Ile	Cys	245	250	255	
Arg	Ser	Arg	Leu	Ala	Asp	Phe	Phe	Thr	Asn	Cys	Gln	Pro	Glu	Ser	Arg				

260					265					270					
Ser	Val	Ser	Asn	Cys	Leu	Lys	Glu	Asn	Tyr	Ala	Asp	Cys	Leu	Leu	Ala
		275					280					285			
Tyr	Ser	Gly	Leu	Ile	Gly	Thr	Val	Met	Thr	Pro	Asn	Tyr	Val	Asp	Ser
	290					295					300				
Ser	Ser	Leu	Ser	Val	Ala	Pro	Trp	Cys	Asp	Cys	Ser	Asn	Ser	Gly	Asn
305					310					315					320
Asp	Leu	Glu	Asp	Cys	Leu	Lys	Phe	Leu	Asn	Phe	Phe	Lys	Asp	Asn	Thr
				325					330					335	
Cys	Leu	Lys	Asn	Ala	Ile	Gln	Ala	Phe	Gly	Asn	Gly	Ser	Asp	Val	Thr
			340					345					350		
Met	Trp	Gln	Pro	Ala	Pro	Pro	Val	Gln	Thr	Thr	Thr	Ala	Thr	Thr	Thr
		355					360					365			
Thr	Ala	Phe	Arg	Val	Lys	Asn	Lys	Pro	Leu	Gly	Pro	Ala	Gly	Ser	Glu
	370					375					380				
Asn	Glu	Ile	Pro	Thr	His	Val	Leu	Pro	Pro	Cys	Ala	Asn	Leu	Gln	Ala
385						390				395					400
Gln	Lys	Leu	Lys	Ser	Asn	Val	Ser	Gly	Ser	Thr	His	Leu	Cys	Leu	Ser
				405					410					415	
Asp	Ser	Asp	Phe	Gly	Lys	Asp	Gly	Leu	Ala	Gly	Ala	Ser	Ser	His	Ile
			420				425						430		
Thr	Thr	Lys	Ser	Met	Ala	Ala	Pro	Pro	Ser	Cys	Ser	Leu	Ser	Ser	Leu
		435					440					445			
Pro	Val	Leu	Met	Leu	Thr	Ala	Leu	Ala	Ala	Leu	Leu	Ser	Val	Ser	Leu
	450					455					460				
Ala	Glu	Thr	Ser												
465															

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AAGGAAAAAA GCGGCCGCCA TGGCGAAGGC GACGTCCGG

39

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

33 AGTTTGTGTCG ACCGTGCGGC ACAGCTCGTC GCA

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 33 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

33 AGTTTGTGTCG ACCGTGCGGC ACAGCGCATC ACA

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1926 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 10..1920

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

48 GCGGCCGCC ATG GCG AAG GCG ACG TCC GGC GCC GCA GGG CTG GGG CTG  
Met Ala Lys Ala Thr Ser Gly Ala Ala Gly Leu Gly Leu  
470 475 480  
96 AAG CTG TTT TTG CTG CTG CCG CTA CTG GGA GAA GCC CCG CTG GGT CTC  
Lys Leu Phe Leu Leu Leu Pro Leu Leu Gly Glu Ala Pro Leu Gly Leu  
485 490 495  
144 TAC TTC TCA AGG GAT GCT TAC TGG GAG AGG CTG TAT GTG GAC CAG CCA  
Tyr Phe Ser Arg Asp Ala Tyr Trp Glu Arg Leu Tyr Val Asp Gln Pro  
500 505 510  
192 GCT GGC ACA CCT CTG CTC TAT GTC CAT GCC CTA CGG GAT GCC CCT GGA



Ala Gly Thr Pro Leu Leu Tyr Val His Ala Leu Arg Asp Ala Pro Gly  
 515 520 525  
 240 GAA GTG CCC AGC TTC CGC CTG GGC CAG TAT CTC TAT GGC GTC TAC CGC  
 Glu Val Pro Ser Phe Arg Leu Gly Gln Tyr Leu Tyr Gly Val Tyr Arg  
 530 535 540 545  
 288 ACG CGT CTG CAT GAG AAT GAC TGG ATC CAC ATC GAT GCG GGC ACT GGC  
 Thr Arg Leu His Glu Asn Asp Trp Ile His Ile Asp Ala Gly Thr Gly  
 550 555 560  
 336 CTC CTC TAC CTC AAT CAG AGC CTG GAC CAT AGT TCC TGG GAG CAG CTC  
 Leu Leu Tyr Leu Asn Gln Ser Leu Asp His Ser Ser Trp Glu Gln Leu  
 565 570 575  
 384 AGC ATC CGA AAT GGC GGC TTC CCC TTG CTC ACC GTC TTC CTC CAG GTC  
 Ser Ile Arg Asn Gly Gly Phe Pro Leu Leu Thr Val Phe Leu Gln Val  
 580 585 590  
 432 TTC CTG GGG TCC ACA GCC CAG AGA GAG GGA GAG TGT CAT TGG CCA GGC  
 Phe Leu Gly Ser Thr Ala Gln Arg Glu Gly Glu Cys His Trp Pro Gly  
 595 600 605  
 480 TGT GCC CGT GTG TAC TTC TCC TTC ATC AAC GAC ACC TTC CCA AAT TGT  
 Cys Ala Arg Val Tyr Phe Ser Phe Ile Asn Asp Thr Phe Pro Asn Cys  
 610 615 620 625  
 528 AGC TCC TTC AAA GCC CGG GAT CTC TGC ACC CCA GAG ACG GGT GTG TCC  
 Ser Ser Phe Lys Ala Arg Asp Leu Cys Thr Pro Glu Thr Gly Val Ser  
 630 635 640  
 576 TTC CGC ATC AGG GAG AAC AGG CCC CCT GGC ACC TTC TAC CAG TTC CGC  
 Phe Arg Ile Arg Glu Asn Arg Pro Pro Gly Thr Phe Tyr Gln Phe Arg  
 645 650 655  
 624 ATG CTA CCT GTG CAG TTC CTT TGT CCT AAC ATC AGT GTG AAG TAC AAA  
 Met Leu Pro Val Gln Phe Leu Cys Pro Asn Ile Ser Val Lys Tyr Lys  
 660 665 670  
 672 CTC TTA GAA GGG GAC GGT CTG CCC TTC CGT TGT GAC CCC GAC TGT CTG  
 Leu Leu Glu Gly Asp Gly Leu Pro Phe Arg Cys Asp Pro Asp Cys Leu  
 675 680 685  
 720 GAG GTG AGC ACG CGG TGG GCA CTG GAT CGG GAG CTT CAG GAG AAG TAT  
 Glu Val Ser Thr Arg Trp Ala Leu Asp Arg Glu Leu Gln Glu Lys Tyr  
 690 695 700 705  
 768 GTG CTG GAG GCT GAG TGC GCA GTG GCA GGC CCT GGA GCC AAC AAG GAG  
 Val Leu Glu Ala Glu Cys Ala Val Ala Gly Pro Gly Ala Asn Lys Glu  
 710 715 720  
 816 AAG GTG GCC GTG TCC TTC CCG GTG ACG GTG TAT GAT GAA GAC GAC TCC

Lys Val Ala Val Ser Phe Pro Val Thr Val Tyr Asp Glu Asp Asp Ser  
 725 730 735  
 864 CCG CCC ACC TTC TCC GGA GGT GTG GGC ACC GCC AGT GCT GTG GTG GAG  
 Pro Pro Thr Phe Ser Gly Gly Val Gly Thr Ala Ser Ala Val Val Glu  
 740 745 750  
 912 TTT AAG CGG AAG GAG GGC ACT GTG GTA GCC ACT CTG CAG GTG TTT GAT  
 Phe Lys Arg Lys Glu Gly Thr Val Val Ala Thr Leu Gln Val Phe Asp  
 755 760 765  
 960 GCA GAT GTG GTG CCA GCA TCT GGG GAG CTG GTG AGG CGG TAC ACA AGC  
 Ala Asp Val Val Pro Ala Ser Gly Glu Leu Val Arg Arg Tyr Thr Ser  
 770 775 780 785  
 1008 ACA CTA CTC TCA GGG GAT TCC TGG GCC CAG CAG ACC TTC CGG GTG GAG  
 Thr Leu Leu Ser Gly Asp Ser Trp Ala Gln Gln Thr Phe Arg Val Glu  
 790 795 800  
 1056 CAC ACA CCC AAC GAG ACC TTG GTC CAG TCC AAC AAC AAC TCC GTG CGG  
 His Thr Pro Asn Glu Thr Leu Val Gln Ser Asn Asn Asn Ser Val Arg  
 805 810 815  
 1104 GCA ACC ATG CAC AAT TAC AAG CTG GTT CTC AAC AGG AGC CTG TCC ATC  
 Ala Thr Met His Asn Tyr Lys Leu Val Leu Asn Arg Ser Leu Ser Ile  
 820 825 830  
 1152 TCA GAG AGC CGA GTC CTG CAG CTA GTA GTC CTG GTC AAT GAC TCA GAC  
 Ser Glu Ser Arg Val Leu Gln Leu Val Val Leu Val Asn Asp Ser Asp  
 835 840 845  
 1200 TTC CAG GGG CCT GGG TCA GGT GGT CTC TTC CTC CAT TTC AAC GTG TCT  
 Phe Gln Gly Pro Gly Ser Gly Val Leu Phe Leu His Phe Asn Val Ser  
 850 855 860 865  
 1248 GTG CTG CCT GTC ACC CTG AAC CTA CCC ATG GCC TAC TCC TTC CCA GTG  
 Val Leu Pro Val Thr Leu Asn Leu Pro Met Ala Tyr Ser Phe Pro Val  
 870 875 880  
 1296 AAT AGG AGA GCC CGC CGT TAT GCC CAG ATT GGG AAA GTT TGC GTG GAG  
 Asn Arg Arg Ala Arg Arg Tyr Ala Gln Ile Gly Lys Val Cys Val Glu  
 885 890 895  
 1344 AAC TGC CAG GAG TTC AGC GGT GTC TCC ATC CAG TAC AAG CTG CAG CCC  
 Asn Cys Gln Glu Phe Ser Gly Val Ser Ile Gln Tyr Lys Leu Gln Pro  
 900 905 910  
 1392 TCC AGC ACC AAC TGC AGT GCC CTA GGT GTG GTC ACC TCA ACA GAA GAC  
 Ser Ser Thr Asn Cys Ser Ala Leu Gly Val Val Thr Ser Thr Glu Asp  
 915 920 925  
 1440 ACC TCA GGG ACC CTA TAT GTA AAT GAC ACG GAG GCC CTG CGG CGA CCT

Thr Ser Gly Thr Leu Tyr Val Asn Asp Thr Glu Ala Leu Arg Arg Pro  
 930 935 940 945  
 GAG TGT ACC GAG CTT CAG TAC ACA GTG GTA GCC ACT GAC CGG CAG ACC  
 1488  
 Glu Cys Thr Glu Leu Gln Tyr Thr Val Val Ala Thr Asp Arg Gln Thr  
 950 955 960  
 CGC AGG CAG ACC CAA GCT TCG TTA GTC GTC ACA GTG GAG GGG ACA TAC  
 1536  
 Arg Arg Gln Thr Gln Ala Ser Leu Val Val Thr Val Glu Gly Thr Tyr  
 965 970 975  
 ATT GCA GAA GAA GTG GGC TGC CCC AAG TCC TGT GCA GTA AAC AAG AGG  
 1584  
 Ile Ala Glu Glu Val Gly Cys Pro Lys Ser Cys Ala Val Asn Lys Arg  
 980 985 990  
 CGA CCT GAG TGT GAG GAG TGT GGT GGC CTG GGT TCT CCA ACT GGC AGA  
 1632  
 Arg Pro Glu Cys Glu Glu Cys Gly Gly Leu Gly Ser Pro Thr Gly Arg  
 995 1000 1005  
 TGT GAG TGG CGT CAG GGA GAT GGT AAA GGG ATC ACC AGG AAC TTC TCC  
 1680  
 Cys Glu Trp Arg Gln Gly Asp Gly Lys Gly Ile Thr Arg Asn Phe Ser  
 1010 1015 1020 1025  
 ACC TGT TCT CCT AGC ACC AGG ACC TGT CCT GAT GGC CAC TGT GAT GCT  
 1728  
 Thr Cys Ser Pro Ser Thr Arg Thr Cys Pro Asp Gly His Cys Asp Ala  
 1030 1035 1040  
 CTG GAG AGC CGG GAT ATC AAC ATT TGC CCC CAG GAC TGT CTC CGT GGC  
 1776  
 Leu Glu Ser Arg Asp Ile Asn Ile Cys Pro Gln Asp Cys Leu Arg Gly  
 1045 1050 1055  
 CCC ATT GTT GGC GGG CAT GAG CGA GGG GAG CGC CAG GGG ATT AAA GCC  
 1824  
 Pro Ile Val Gly Gly His Glu Arg Gly Glu Arg Gln Gly Ile Lys Ala  
 1060 1065 1070  
 GGC TAT GGC ATC TGC AAC TGT TTC CCT GAT GAG AAG AAG TGC TTC TGC  
 1872  
 Gly Tyr Gly Ile Cys Asn Cys Phe Pro Asp Glu Lys Lys Cys Phe Cys  
 1075 1080 1085  
 GAG CCA GAG GAC AGC CAG GGC CCA TTG TGT GAT GCG CTG TGC CGC ACG  
 1920  
 Glu Pro Glu Asp Ser Gln Gly Pro Leu Cys Asp Ala Leu Cys Arg Thr  
 1090 1095 1100 1105  
 GTCGAC  
 1926

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 637 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Ala Lys Ala Thr Ser Gly Ala Ala Gly Leu Gly Leu Lys Leu Phe  
1 5 10 15  
Leu Leu Leu Pro Leu Leu Gly Glu Ala Pro Leu Gly Leu Tyr Phe Ser  
20 25 30  
Arg Asp Ala Tyr Trp Glu Arg Leu Tyr Val Asp Gln Pro Ala Gly Thr  
35 40 45  
Pro Leu Leu Tyr Val His Ala Leu Arg Asp Ala Pro Gly Glu Val Pro  
50 55 60  
Ser Phe Arg Leu Gly Gln Tyr Leu Tyr Gly Val Tyr Arg Thr Arg Leu  
65 70 75 80  
His Glu Asn Asp Trp Ile His Ile Asp Ala Gly Thr Gly Leu Leu Tyr  
85 90 95  
Leu Asn Gln Ser Leu Asp His Ser Ser Trp Glu Gln Leu Ser Ile Arg  
100 105 110  
Asn Gly Gly Phe Pro Leu Leu Thr Val Phe Leu Gln Val Phe Leu Gly  
115 120 125  
Ser Thr Ala Gln Arg Glu Gly Glu Cys His Trp Pro Gly Cys Ala Arg  
130 135 140  
Val Tyr Phe Ser Phe Ile Asn Asp Thr Phe Pro Asn Cys Ser Ser Phe  
145 150 155 160  
Lys Ala Arg Asp Leu Cys Thr Pro Glu Thr Gly Val Ser Phe Arg Ile  
165 170 175  
Arg Glu Asn Arg Pro Pro Gly Thr Phe Tyr Gln Phe Arg Met Leu Pro  
180 185 190  
Val Gln Phe Leu Cys Pro Asn Ile Ser Val Lys Tyr Lys Leu Leu Glu  
195 200 205  
Gly Asp Gly Leu Pro Phe Arg Cys Asp Pro Asp Cys Leu Glu Val Ser  
210 215 220  
Thr Arg Trp Ala Leu Asp Arg Glu Leu Gln Glu Lys Tyr Val Leu Glu  
225 230 235 240  
Ala Glu Cys Ala Val Ala Gly Pro Gly Ala Asn Lys Glu Lys Val Ala  
245 250 255  
Val Ser Phe Pro Val Thr Val Tyr Asp Glu Asp Asp Ser Pro Pro Thr  
260 265 270  
Phe Ser Gly Gly Val Gly Thr Ala Ser Ala Val Val Glu Phe Lys Arg  
275 280 285  
Lys Glu Gly Thr Val Val Ala Thr Leu Gln Val Phe Asp Ala Asp Val  
290 295 300  
Val Pro Ala Ser Gly Glu Leu Val Arg Arg Tyr Thr Ser Thr Leu Leu  
305 310 315 320  
Ser Gly Asp Ser Trp Ala Gln Gln Thr Phe Arg Val Glu His Thr Pro  
325 330 335

Asn Glu Thr Leu Val Gln Ser Asn Asn Asn Ser Val Arg Ala Thr Met  
 340 345 350  
 His Asn Tyr Lys Leu Val Leu Asn Arg Ser Leu Ser Ile Ser Glu Ser  
 355 360 365  
 Arg Val Leu Gln Leu Val Val Leu Val Asn Asp Ser Asp Phe Gln Gly  
 370 375 380  
 Pro Gly Ser Gly Val Leu Phe Leu His Phe Asn Val Ser Val Leu Pro  
 385 390 395 400  
 Val Thr Leu Asn Leu Pro Met Ala Tyr Ser Phe Pro Val Asn Arg Arg  
 405 410 415  
 Ala Arg Arg Tyr Ala Gln Ile Gly Lys Val Cys Val Glu Asn Cys Gln  
 420 425 430  
 Glu Phe Ser Gly Val Ser Ile Gln Tyr Lys Leu Gln Pro Ser Ser Thr  
 435 440 445  
 Asn Cys Ser Ala Leu Gly Val Val Thr Ser Thr Glu Asp Thr Ser Gly  
 450 455 460  
 Thr Leu Tyr Val Asn Asp Thr Glu Ala Leu Arg Arg Pro Glu Cys Thr  
 465 470 475 480  
 Glu Leu Gln Tyr Thr Val Val Ala Thr Asp Arg Gln Thr Arg Arg Gln  
 485 490 495  
 Thr Gln Ala Ser Leu Val Val Thr Val Glu Gly Thr Tyr Ile Ala Glu  
 500 505 510  
 Glu Val Gly Cys Pro Lys Ser Cys Ala Val Asn Lys Arg Arg Pro Glu  
 515 520 525  
 Cys Glu Glu Cys Gly Gly Leu Gly Ser Pro Thr Gly Arg Cys Glu Trp  
 530 535 540  
 Arg Gln Gly Asp Gly Lys Gly Ile Thr Arg Asn Phe Ser Thr Cys Ser  
 545 550 555 560  
 Pro Ser Thr Arg Thr Cys Pro Asp Gly His Cys Asp Ala Leu Glu Ser  
 565 570 575  
 Arg Asp Ile Asn Ile Cys Pro Gln Asp Cys Leu Arg Gly Pro Ile Val  
 580 585 590  
 Gly Gly His Glu Arg Gly Glu Arg Gln Gly Ile Lys Ala Gly Tyr Gly  
 595 600 605  
 Ile Cys Asn Cys Phe Pro Asp Glu Lys Lys Cys Phe Cys Glu Pro Glu  
 610 615 620  
 Asp Ser Gln Gly Pro Leu Cys Asp Ala Leu Cys Arg Thr  
 625 630 635

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1223 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..1038

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```
48  CTG CTG GAG GAT TCC CCA TAT GAA CCA GTT AAC AGC AGA TTG TCA GAT
    Leu Leu Glu Asp Ser Pro Tyr Glu Pro Val Asn Ser Arg Leu Ser Asp
        640                645                650
96  ATA TTC CGG GTG GTC CCA TTC ATA TCA GTG GAG CAC ATT CCC AAA GGG
    Ile Phe Arg Val Val Pro Phe Ile Ser Val Glu His Ile Pro Lys Gly
        655                660                665
144 AAC AAC TGC CTG GAT GCA GCG AAG GCC TGC AAC CTC GAC GAC ATT TGC
    Asn Asn Cys Leu Asp Ala Ala Lys Ala Cys Asn Leu Asp Asp Ile Cys
        670                675                680                685
192 AAG AAG TAC AGG TCG GCG TAC ATC ACC CCG TGC ACC ACC AGC GTG TCC
    Lys Lys Tyr Arg Ser Ala Tyr Ile Thr Pro Cys Thr Thr Ser Val Ser
        690                695                700
240 AAC GAT GTC TGC AAC CGC CGC AAG TGC CAC AAG GCC CTC CGG CAG TTC
    Asn Asp Val Cys Asn Arg Arg Lys Cys His Lys Ala Leu Arg Gln Phe
        705                710                715
288 TTT GAC AAG GTC CCG GCC AAG CAC AGC TAC GGA ATG CTC TTC TGC TCC
    Phe Asp Lys Val Pro Ala Lys His Ser Tyr Gly Met Leu Phe Cys Ser
        720                725                730
336 TGC CGG GAC ATC GCC TGC ACA GAG CGG AGG CGA CAG ACC ATC GTG CCT
    Cys Arg Asp Ile Ala Cys Thr Glu Arg Arg Arg Gln Thr Ile Val Pro
        735                740                745
384 GTG TGC TCC TAT GAA GAG AGG GAG AAG CCC AAC TGT TTG AAT TTG CAG
    Val Cys Ser Tyr Glu Glu Arg Glu Lys Pro Asn Cys Leu Asn Leu Gln
        750                755                760                765
432 GAC TCC TGC AAG ACG AAT TAC ATC TGC AGA TCT CGC CTT GCG GAT TTT
    Asp Ser Cys Lys Thr Asn Tyr Ile Cys Arg Ser Arg Leu Ala Asp Phe
        770                775                780
480 TTT ACC AAC TGC CAG CCA GAG TCA AGG TCT GTC AGC AGC TGT CTA AAG
    Phe Thr Asn Cys Gln Pro Glu Ser Arg Ser Val Ser Ser Cys Leu Lys
        785                790                795
528 GAA AAC TAC GCT GAC TGC CTC CTC GCC TAC TCG GGG CTT ATT GGC ACA
    Glu Asn Tyr Ala Asp Cys Leu Leu Ala Tyr Ser Gly Leu Ile Gly Thr
        800                805                810
```

576 GTC ATG ACC CCC AAC TAC ATA GAC TCC AGT AGC CTC AGT GTG GCC CCA  
 Val Met Thr Pro Asn Tyr Ile Asp Ser Ser Ser Leu Ser Val Ala Pro  
 815 820 825  
 624 TGG TGT GAC TGC AGC AAC AGT GGG AAC GAC CTA GAA GAG TGC TTG AAA  
 Trp Cys Asp Cys Ser Asn Ser Gly Asn Asp Leu Glu Glu Cys Leu Lys  
 830 835 840 845  
 672 TTT TTG AAT TTC TTC AAG GAC AAT ACA TGT CTT AAA AAT GCA ATT CAA  
 Phe Leu Asn Phe Phe Lys Asp Asn Thr Cys Leu Lys Asn Ala Ile Gln  
 850 855 860  
 720 GCC TTT GGC AAT GGC TCC GAT GTG ACC GTG TGG CAG CCA GCC TTC CCA  
 Ala Phe Gly Asn Gly Ser Asp Val Thr Val Trp Gln Pro Ala Phe Pro  
 865 870 875  
 768 GTA CAG ACC ACC ACT GCC ACT ACC ACC ACT GCC CTC CGG GTT AAG AAC  
 Val Gln Thr Thr Thr Ala Thr Thr Thr Thr Ala Leu Arg Val Lys Asn  
 880 885 890  
 816 AAG CCC CTG GGG CCA GCA GGG TCT GAG AAT GAA ATT CCC ACT CAT GTT  
 Lys Pro Leu Gly Pro Ala Gly Ser Glu Asn Glu Ile Pro Thr His Val  
 895 900 905  
 864 TTG CCA CCG TGT GCA AAT TTA CAG GCA CAG AAG CTG AAA TCC AAT GTG  
 Leu Pro Pro Cys Ala Asn Leu Gln Ala Gln Lys Leu Lys Ser Asn Val  
 910 915 920 925  
 912 TCG GGC AAT ACA CAC CTC TGT ATT TCC AAT GGT AAT TAT GAA AAA GAA  
 Ser Gly Asn Thr His Leu Cys Ile Ser Asn Gly Asn Tyr Glu Lys Glu  
 930 935 940  
 960 GGT CTC GGT GCT TCC AGC CAC ATA ACC ACA AAA TCA ATG GCT GCT CCT  
 Gly Leu Gly Ala Ser Ser His Ile Thr Thr Lys Ser Met Ala Ala Pro  
 945 950 955  
 1008 CCA AGC TGT GGT CTG AGC CCA CTG CTG GTC CTG GTG GTA ACC GCT CTG  
 Pro Ser Cys Gly Leu Ser Pro Leu Leu Val Leu Val Val Thr Ala Leu  
 960 965 970  
 1058 TCC ACC CTA TTA TCT TTA ACA GAA ACA TCA TAGCTGCATT AAAAAAATAC  
 Ser Thr Leu Leu Ser Leu Thr Glu Thr Ser  
 975 980  
 1118 AATATGGACA TGTA AAAAGA CAAAAACCAA GTTATCTGTT TCCTGTTCTC TTGTATAGCT  
 1178 GAAATTCCAG TTTAGGAGCT CAGTTGAGAA ACAGTTCCAT TCAACTGGAA CATTTTTTTT  
 1223 TTTTCCTTTT AAGAAAGCTT CTTGTGATCC TTCGGGGCTT CTGTG

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 346 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Leu Leu Glu Asp Ser Pro Tyr Glu Pro Val Asn Ser Arg Leu Ser Asp  
1 5 10 15  
Ile Phe Arg Val Val Pro Phe Ile Ser Val Glu His Ile Pro Lys Gly  
20 25 30  
Asn Asn Cys Leu Asp Ala Ala Lys Ala Cys Asn Leu Asp Asp Ile Cys  
35 40 45  
Lys Lys Tyr Arg Ser Ala Tyr Ile Thr Pro Cys Thr Thr Ser Val Ser  
50 55 60  
Asn Asp Val Cys Asn Arg Arg Lys Cys His Lys Ala Leu Arg Gln Phe  
65 70 75 80  
Phe Asp Lys Val Pro Ala Lys His Ser Tyr Gly Met Leu Phe Cys Ser  
85 90 95  
Cys Arg Asp Ile Ala Cys Thr Glu Arg Arg Arg Gln Thr Ile Val Pro  
100 105 110  
Val Cys Ser Tyr Glu Glu Arg Glu Lys Pro Asn Cys Leu Asn Leu Gln  
115 120 125  
Asp Ser Cys Lys Thr Asn Tyr Ile Cys Arg Ser Arg Leu Ala Asp Phe  
130 135 140  
Phe Thr Asn Cys Gln Pro Glu Ser Arg Ser Val Ser Ser Cys Leu Lys  
145 150 155 160  
Glu Asn Tyr Ala Asp Cys Leu Leu Ala Tyr Ser Gly Leu Ile Gly Thr  
165 170 175  
Val Met Thr Pro Asn Tyr Ile Asp Ser Ser Ser Leu Ser Val Ala Pro  
180 185 190  
Trp Cys Asp Cys Ser Asn Ser Gly Asn Asp Leu Glu Glu Cys Leu Lys  
195 200 205  
Phe Leu Asn Phe Phe Lys Asp Asn Thr Cys Leu Lys Asn Ala Ile Gln  
210 215 220  
Ala Phe Gly Asn Gly Ser Asp Val Thr Val Trp Gln Pro Ala Phe Pro  
225 230 235 240  
Val Gln Thr Thr Thr Ala Thr Thr Thr Thr Ala Leu Arg Val Lys Asn  
245 250 255  
Lys Pro Leu Gly Pro Ala Gly Ser Glu Asn Glu Ile Pro Thr His Val  
260 265 270  
Leu Pro Pro Cys Ala Asn Leu Gln Ala Gln Lys Leu Lys Ser Asn Val  
275 280 285



Ser Gly Asn Thr His Leu Cys Ile Ser Asn Gly Asn Tyr Glu Lys Glu  
 290 295 300  
 Gly Leu Gly Ala Ser Ser His Ile Thr Thr Lys Ser Met Ala Ala Pro  
 305 310 315 320  
 Pro Ser Cys Gly Leu Ser Pro Leu Leu Val Leu Val Val Thr Ala Leu  
 325 330 335  
 Ser Thr Leu Leu Ser Leu Thr Glu Thr Ser  
 340 345

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1682 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 118..1497

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGGCGGCCAG AGCAGCACAG CTGTCCGGGG ATCGCTGCAT GCTGAGCTCC CTCGGCAAGA  
 60  
 CCCAGCGGCG GCTCGGGATT TTTTGGGGG GCGGGGACC AGCCCCGCGC CGGCACC  
 117  
 ATG TTC CTG GCG ACC CTG TAC TTC GCG CTG CCG CTC TTG GAC TTG CTC  
 165  
 Met Phe Leu Ala Thr Leu Tyr Phe Ala Leu Pro Leu Leu Asp Leu Leu  
 350 355 360  
 CTG TCG GCC GAA GTG AGC GGC GGA GAC CGC CTG GAT TGC GTG AAA GCC  
 213  
 Leu Ser Ala Glu Val Ser Gly Gly Asp Arg Leu Asp Cys Val Lys Ala  
 365 370 375  
 AGT GAT CAG TGC CTG AAG GAG CAG AGC TGC AGC ACC AAG TAC CGC ACG  
 261  
 Ser Asp Gln Cys Leu Lys Glu Gln Ser Cys Ser Thr Lys Tyr Arg Thr  
 380 385 390  
 CTA AGG CAG TGC GTG GCG GGC AAG GAG ACC AAC TTC AGC CTG GCA TCC  
 309  
 Leu Arg Gln Cys Val Ala Gly Lys Glu Thr Asn Phe Ser Leu Ala Ser  
 395 400 405 410  
 GGC CTG GAG GCC AAG GAT GAG TGC CGC AGC GCC ATG GAG GCC CTG AAG  
 357  
 Gly Leu Glu Ala Lys Asp Glu Cys Arg Ser Ala Met Glu Ala Leu Lys  
 415 420 425  
 CAG AAG TCG CTC TAC AAC TGC CGC TGC AAG CGG GGT ATG AAG AAG GAG  
 405  
 Gln Lys Ser Leu Tyr Asn Cys Arg Cys Lys Arg Gly Met Lys Lys Glu

	430	435	440
453	AAG AAC TGC CTG CGC ATT TAC	TGG AGC ATG TAC CAG AGC CTG CAG GGA	
	Lys Asn Cys Leu Arg Ile Tyr Trp Ser Met Tyr Gln Ser Leu Gln Gly		
	445	450	455
501	AAT GAT CTG CTG GAG GAT TCC CCA TAT GAA CCA GTT AAC AGC AGA TTG		
	Asn Asp Leu Leu Glu Asp Ser Pro Tyr Glu Pro Val Asn Ser Arg Leu		
	460	465	470
549	TCA GAT ATA TTC CGG GTG GTC CCA TTC ATA TCA GTG GAG CAC ATT CCC		
	Ser Asp Ile Phe Arg Val Val Pro Phe Ile Ser Val Glu His Ile Pro		
	475	480	485
597	AAA GGG AAC AAC TGC CTG GAT GCA GCG AAG GCC TGC AAC CTC GAC GAC		
	Lys Gly Asn Asn Cys Leu Asp Ala Ala Lys Ala Cys Asn Leu Asp Asp		
	495	500	505
645	ATT TGC AAG AAG TAC AGG TCG GCG TAC ATC ACC CCG TGC ACC ACC AGC		
	Ile Cys Lys Lys Tyr Arg Ser Ala Tyr Ile Thr Pro Cys Thr Thr Ser		
	510	515	520
693	GTG TCC AAC GAT GTC TGC AAC CGC CGC AAG TGC CAC AAG GCC CTC CGG		
	Val Ser Asn Asp Val Cys Asn Arg Arg Lys Cys His Lys Ala Leu Arg		
	525	530	535
741	CAG TTC TTT GAC AAG GTC CCG GCC AAG CAC AGC TAC GGA ATG CTC TTC		
	Gln Phe Phe Asp Lys Val Pro Ala Lys His Ser Tyr Gly Met Leu Phe		
	540	545	550
789	TGC TCC TGC CGG GAC ATC GCC TGC ACA GAG CGG AGG CGA CAG ACC ATC		
	Cys Ser Cys Arg Asp Ile Ala Cys Thr Glu Arg Arg Arg Gln Thr Ile		
	555	560	565
837	GTG CCT GTG TGC TCC TAT GAA GAG AGG GAG AAG CCC AAC TGT TTG AAT		
	Val Pro Val Cys Ser Tyr Glu Glu Arg Glu Lys Pro Asn Cys Leu Asn		
	575	580	585
885	TTG CAG GAC TCC TGC AAG ACG AAT TAC ATC TGC AGA TCT CGC CTT GCG		
	Leu Gln Asp Ser Cys Lys Thr Asn Tyr Ile Cys Arg Ser Arg Leu Ala		
	590	595	600
933	GAT TTT TTT ACC AAC TGC CAG CCA GAG TCA AGG TCT GTC AGC AGC TGT		
	Asp Phe Phe Thr Asn Cys Gln Pro Glu Ser Arg Ser Val Ser Ser Cys		
	605	610	615
981	CTA AAG GAA AAC TAC GCT GAC TGC CTC CTC GCC TAC TCG GGG CTT ATT		
	Leu Lys Glu Asn Tyr Ala Asp Cys Leu Leu Ala Tyr Ser Gly Leu Ile		
	620	625	630
1029	GGC ACA GTC ATG ACC CCC AAC TAC ATA GAC TCC AGT AGC CTC AGT GTG		
	Gly Thr Val Met Thr Pro Asn Tyr Ile Asp Ser Ser Ser Leu Ser Val		

635	640	645	650
1077	GCC CCA TGG TGT GAC TGC AGC AAC AGT GGG AAC GAC CTA GAA GAG TGC		
	Ala Pro Trp Cys Asp Cys Ser Asn Ser Gly Asn Asp Leu Glu Glu Cys	660	665
1125	TTG AAA TTT TTG AAT TTC TTC AAG GAC AAT ACA TGT CTT AAA AAT GCA		
	Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr Cys Leu Lys Asn Ala	670	680
1173	ATT CAA GCC TTT GGC AAT GGC TCC GAT GTG ACC GTG TGG CAG CCA GCC		
	Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr Val Trp Gln Pro Ala	685	695
1221	TTC CCA GTA CAG ACC ACC ACT GCC ACT ACC ACC ACT GCC CTC CGG GTT		
	Phe Pro Val Gln Thr Thr Thr Ala Thr Thr Thr Thr Ala Leu Arg Val	700	710
1269	AAG AAC AAG CCC CTG GGG CCA GCA GGG TCT GAG AAT GAA ATT CCC ACT		
	Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser Glu Asn Glu Ile Pro Thr	715	730
1317	CAT GTT TTG CCA CCG TGT GCA AAT TTA CAG GCA CAG AAG CTG AAA TCC		
	His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala Gln Lys Leu Lys Ser	735	745
1365	AAT GTG TCG GGC AAT ACA CAC CTC TGT ATT TCC AAT GGT AAT TAT GAA		
	Asn Val Ser Gly Asn Thr His Leu Cys Ile Ser Asn Gly Asn Tyr Glu	750	760
1413	AAA GAA GGT CTC GGT GCT TCC AGC CAC ATA ACC ACA AAA TCA ATG GCT		
	Lys Glu Gly Leu Gly Ala Ser Ser His Ile Thr Thr Lys Ser Met Ala	765	775
1461	GCT CCT CCA AGC TGT GGT CTG AGC CCA CTG CTG GTC CTG GTG GTA ACC		
	Ala Pro Pro Ser Cys Gly Leu Ser Pro Leu Leu Val Leu Val Val Thr	780	790
1507	GCT CTG TCC ACC CTA TTA TCT TTA ACA GAA ACA TCA TAGCTGCATT		
	Ala Leu Ser Thr Leu Leu Ser Leu Thr Glu Thr Ser	795	805
1567	AAAAAAATAC AATATGGACA TGTA AAAAGA CAAAAACCAA GTTATCTGTT TCCTGTCTC		
1627	TTGTATAGCT GAAATTCAG TTTAGGAGCT CAGTTGAGAA ACAGTCCAT TCAACTGGAA		
1682	CATTTTTTTT TTTTCCTTTT AAGAAAGCTT CTTGTGATCC TTCGGGGCTT CTGTG		

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 460 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

```

Met Phe Leu Ala Thr Leu Tyr Phe Ala Leu Pro Leu Leu Asp Leu Leu
 1           5           10           15
Leu Ser Ala Glu Val Ser Gly Gly Asp Arg Leu Asp Cys Val Lys Ala
          20           25           30
Ser Asp Gln Cys Leu Lys Glu Gln Ser Cys Ser Thr Lys Tyr Arg Thr
          35           40           45
Leu Arg Gln Cys Val Ala Gly Lys Glu Thr Asn Phe Ser Leu Ala Ser
          50           55           60
Gly Leu Glu Ala Lys Asp Glu Cys Arg Ser Ala Met Glu Ala Leu Lys
          65           70           75           80
Gln Lys Ser Leu Tyr Asn Cys Arg Cys Lys Arg Gly Met Lys Lys Glu
          85           90           95
Lys Asn Cys Leu Arg Ile Tyr Trp Ser Met Tyr Gln Ser Leu Gln Gly
          100          105          110
Asn Asp Leu Leu Glu Asp Ser Pro Tyr Glu Pro Val Asn Ser Arg Leu
          115          120          125
Ser Asp Ile Phe Arg Val Val Pro Phe Ile Ser Val Glu His Ile Pro
          130          135          140
Lys Gly Asn Asn Cys Leu Asp Ala Ala Lys Ala Cys Asn Leu Asp Asp
          145          150          155          160
Ile Cys Lys Lys Tyr Arg Ser Ala Tyr Ile Thr Pro Cys Thr Thr Ser
          165          170          175
Val Ser Asn Asp Val Cys Asn Arg Arg Lys Cys His Lys Ala Leu Arg
          180          185          190
Gln Phe Phe Asp Lys Val Pro Ala Lys His Ser Tyr Gly Met Leu Phe
          195          200          205
Cys Ser Cys Arg Asp Ile Ala Cys Thr Glu Arg Arg Arg Gln Thr Ile
          210          215          220
Val Pro Val Cys Ser Tyr Glu Glu Arg Glu Lys Pro Asn Cys Leu Asn
          225          230          235          240
Leu Gln Asp Ser Cys Lys Thr Asn Tyr Ile Cys Arg Ser Arg Leu Ala
          245          250          255
Asp Phe Phe Thr Asn Cys Gln Pro Glu Ser Arg Ser Val Ser Ser Cys
          260          265          270
Leu Lys Glu Asn Tyr Ala Asp Cys Leu Leu Ala Tyr Ser Gly Leu Ile
          275          280          285
Gly Thr Val Met Thr Pro Asn Tyr Ile Asp Ser Ser Ser Leu Ser Val
          290          295          300

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Ala Pro Trp Cys Asp Cys Ser Asn Ser Gly Asn Asp Leu Glu Glu Cys  
305 310 315 320

Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr Cys Leu Lys Asn Ala  
325 330 335

Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr Val Trp Gln Pro Ala  
340 345 350

Phe Pro Val Gln Thr Thr Thr Ala Thr Thr Thr Thr Ala Leu Arg Val  
355 360 365

Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser Glu Asn Glu Ile Pro Thr  
370 375 380

His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala Gln Lys Leu Lys Ser  
385 390 395 400

Asn Val Ser Gly Asn Thr His Leu Cys Ile Ser Asn Gly Asn Tyr Glu  
405 410 415

Lys Glu Gly Leu Gly Ala Ser Ser His Ile Thr Thr Lys Ser Met Ala  
420 425 430

Ala Pro Pro Ser Cys Gly Leu Ser Pro Leu Leu Val Leu Val Val Thr  
435 440 445

Ala Leu Ser Thr Leu Leu Ser Leu Thr Glu Thr Ser  
450 455 460

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1888 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 25..1416

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

51 AAAAAACGGT GGGATTTATT TAAC ATG ATC TTG GCA AAC GTC TTC TGC CTC  
Met Ile Leu Ala Asn Val Phe Cys Leu  
465

99 TTC TTC TTT CTA GAC GAG ACC CTC CGC TCT TTG GCC AGC CCT TCC TCC  
Phe Phe Phe Leu Asp Glu Thr Leu Arg Ser Leu Ala Ser Pro Ser Ser  
470 475 480 485

147 CTG CAG GGC CCC GAG CTC CAC GGC TGG CGC CCC CCA GTG GAC TGT GTC  
Leu Gln Gly Pro Glu Leu His Gly Trp Arg Pro Pro Val Asp Cys Val  
490 495 500

195 CGG GCC AAT GAG CTG TGT GCC GCC GAA TCC AAC TGC AGC TCT CGC TAC

Arg Ala Asn Glu Leu Cys Ala Ala Glu Ser Asn Cys Ser Ser Arg Tyr  
 505 510 515  
 243 CGC ACT CTG CGG CAG TGC CTG GCA GGC CGC GAC CGC AAC ACC ATG CTG  
 Arg Thr Leu Arg Gln Cys Leu Ala Gly Arg Asp Arg Asn Thr Met Leu  
 520 525 530  
 291 GCC AAC AAG GAG TGC CAG GCG GCC TTG GAG GTC TTG CAG GAG AGC CCG  
 Ala Asn Lys Glu Cys Gln Ala Ala Leu Glu Val Leu Gln Glu Ser Pro  
 535 540 545  
 339 CTG TAC GAC TGC CGC TGC AAG CGG GGC ATG AAG AAG GAG CTG CAG TGT  
 Leu Tyr Asp Cys Arg Cys Lys Arg Gly Met Lys Lys Glu Leu Gln Cys  
 550 555 560 565  
 387 CTG CAG ATC TAC TGG AGC ATC CAC CTG GGG CTG ACC GAG GGT GAG GAG  
 Leu Gln Ile Tyr Trp Ser Ile His Leu Gly Leu Thr Glu Gly Glu Glu  
 570 575 580  
 435 TTC TAC GAA GCC TCC CCC TAT GAG CCG GTG ACC TCC CGC CTC TCG GAC  
 Phe Tyr Glu Ala Ser Pro Tyr Glu Pro Val Thr Ser Arg Leu Ser Asp  
 585 590 595  
 483 ATC TTC AGG CTT GCT TCA ATC TTC TCA GGG ACA GGG GCA GAC CCG GTG  
 Ile Phe Arg Leu Ala Ser Ile Phe Ser Gly Thr Gly Ala Asp Pro Val  
 600 605 610  
 531 GTC AGC GCC AAG AGC AAC CAT TGC CTG GAT GCT GCC AAG GCC TGC AAC  
 Val Ser Ala Lys Ser Asn His Cys Leu Asp Ala Ala Lys Ala Cys Asn  
 615 620 625  
 579 CTG AAT GAC AAC TGC AAG AAG CTG CGC TCC TCC TAC ATC TCC ATC TGC  
 Leu Asn Asp Asn Cys Lys Lys Leu Arg Ser Ser Tyr Ile Ser Ile Cys  
 630 635 640 645  
 627 AAC CGC GAG ATC TCG CCC ACC GAG CGC TGC AAC CGC CGC AAG TGC CAC  
 Asn Arg Glu Ile Ser Pro Thr Glu Arg Cys Asn Arg Arg Lys Cys His  
 650 655 660  
 675 AAG GCC CTG CGC CAG TTC TTC GAC CGG GTG CCC AGC GAG TAC ACC TAC  
 Lys Ala Leu Arg Gln Phe Phe Asp Arg Val Pro Ser Glu Tyr Thr Tyr  
 665 670 675  
 723 CGC ATG CTC TTC TGC TCC TGC CAA GAC CAG GCG TGC GCT GAG CGC CGC  
 Arg Met Leu Phe Cys Ser Cys Gln Asp Gln Ala Cys Ala Glu Arg Arg  
 680 685 690  
 771 CGG CAA ACC ATC CTG CCC AGC TGC TCC TAT GAG GAC AAG GAG AAG CCC  
 Arg Gln Thr Ile Leu Pro Ser Cys Ser Tyr Glu Asp Lys Glu Lys Pro  
 695 700 705  
 819 AAC TGC CTG GAC CTG CGT GGC GTG TGC CGG ACT GAC CAC CTG TGT CGG

Asn Cys Leu Asp Leu Arg Gly Val Cys Arg Thr Asp His Leu Cys Arg  
 710 715 720 725  
 867 TCC CGG CTG GCC GAC TTC CAT GCC AAT TGT CGA GCC TCC TAC CAG ACG  
 Ser Arg Leu Ala Asp Phe His Ala Asn Cys Arg Ala Ser Tyr Gln Thr  
 730 735 740  
 915 GTC ACC AGC TGC CCT GCG GAC AAT TAC CAG GCG TGT CTG GGC TCT TAT  
 Val Thr Ser Cys Pro Ala Asp Asn Tyr Gln Ala Cys Leu Gly Ser Tyr  
 745 750 755  
 963 GCT GGC ATG ATT GGG TTT GAC ATG ACA CCT AAC TAT GTG GAC TCC AGC  
 Ala Gly Met Ile Gly Phe Asp Met Thr Pro Asn Tyr Val Asp Ser Ser  
 760 765 770  
 1011 CCC ACT GGC ATC GTG GTG TCC CCC TGG TGC AGC TGT CGT GGC AGC GGG  
 Pro Thr Gly Ile Val Val Ser Pro Trp Cys Ser Cys Arg Gly Ser Gly  
 775 780 785  
 1059 AAC ATG GAG GAG GAG TGT GAG AAG TTC CTC AGG GAC TTC ACC GAG AAC  
 Asn Met Glu Glu Glu Cys Glu Lys Phe Leu Arg Asp Phe Thr Glu Asn  
 790 795 800 805  
 1107 CCA TGC CTC CGG AAC GCC ATC CAG GCC TTT GGC AAC GGC ACG GAC GTG  
 Pro Cys Leu Arg Asn Ala Ile Gln Ala Phe Gly Asn Gly Thr Asp Val  
 810 815 820  
 1155 AAC GTG TCC CCA AAA GGC CCC TCG TTC CAG GCC ACC CAG GCC CCT CGG  
 Asn Val Ser Pro Lys Gly Pro Ser Phe Gln Ala Thr Gln Ala Pro Arg  
 825 830 835  
 1203 GTG GAG AAG ACG CCT TCT TTG CCA GAT GAC CTC AGT GAC AGT ACC AGC  
 Val Glu Lys Thr Pro Ser Leu Pro Asp Asp Leu Ser Asp Ser Thr Ser  
 840 845 850  
 1251 TTG GGG ACC AGT GTC ATC ACC ACC TGC ACG TCT GTC CAG GAG CAG GGG  
 Leu Gly Thr Ser Val Ile Thr Thr Cys Thr Ser Val Gln Glu Gln Gly  
 855 860 865  
 1299 CTG AAG GCC AAC AAC TCC AAA GAG TTA AGC ATG TGC TTC ACA GAG CTC  
 Leu Lys Ala Asn Asn Ser Lys Glu Leu Ser Met Cys Phe Thr Glu Leu  
 870 875 880 885  
 1347 ACG ACA AAT ATC ATC CCA GGG AGT AAC AAG GTG ATC AAA CCT AAC TCA  
 Thr Thr Asn Ile Ile Pro Gly Ser Asn Lys Val Ile Lys Pro Asn Ser  
 890 895 900  
 1395 GGC CCC AGC AGA GCC AGA CCG TCG GCT GCC TTG ACC GTG CTG TCT GTC  
 Gly Pro Ser Arg Ala Arg Pro Ser Ala Ala Leu Thr Val Leu Ser Val  
 905 910 915  
 1446 CTG ATG CTG AAA CTG GCC TTG TAGGCTGTGG GAACCGAGTC AGAAGATTTT

Leu Met Leu Lys Leu Ala Leu  
920

1506 TGAAAGCTAC GCAGACAAGA ACAGCCGCCT GACGAAATGG AAACACACAC AGACACACAC  
1566 ACACCTTGCA AAAAAAAAAAT TGTTTTTCCTT ACCTTGTCGC TGAACCTGTC TCCTCCCAGG  
1626 TTTCTTCTCT GGAGAAGTTT TTGTAAACCA AACAGACAAG CAGGCAGGCA GCCTGAGAGC  
1686 TGGCCCAGGG GTCCCCTGGC AGGGGAAACT CTGGTGCCGG GGAGGGCACG AGGCTCTAGA  
1746 AATGCCCTTC ACTTTCTCCT GGTGTTTTTC TCTCTGGACC CTTCTGAAGC AGAGACCGGA  
1806 CAAGAGCCTG CAGCGGAAGG GACTCTGGGC TGTGCCTGAG GCTGGCTGGG GGCAGGACAA  
1866 CACAGCTGCT TCCCCAGGCT GCCCACTCTG GGGACCCGCT GGGGGCTGGC AGAGGGCATC  
1888 GGTCAGCGGG GCAGCGGGGC TG

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 464 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met	Ile	Leu	Ala	Asn	Val	Phe	Cys	Leu	Phe	Phe	Phe	Leu	Asp	Glu	Thr
1				5				10						15	
Leu	Arg	Ser	Leu	Ala	Ser	Pro	Ser	Ser	Leu	Gln	Gly	Pro	Glu	Leu	His
			20					25						30	
Gly	Trp	Arg	Pro	Pro	Val	Asp	Cys	Val	Arg	Ala	Asn	Glu	Leu	Cys	Ala
			35				40					45			
Ala	Glu	Ser	Asn	Cys	Ser	Ser	Arg	Tyr	Arg	Thr	Leu	Arg	Gln	Cys	Leu
	50					55					60				
Ala	Gly	Arg	Asp	Arg	Asn	Thr	Met	Leu	Ala	Asn	Lys	Glu	Cys	Gln	Ala
	65				70					75					80
Ala	Leu	Glu	Val	Leu	Gln	Glu	Ser	Pro	Leu	Tyr	Asp	Cys	Arg	Cys	Lys
			85						90					95	
Arg	Gly	Met	Lys	Lys	Glu	Leu	Gln	Cys	Leu	Gln	Ile	Tyr	Trp	Ser	Ile
			100					105					110		
His	Leu	Gly	Leu	Thr	Glu	Gly	Glu	Glu	Phe	Tyr	Glu	Ala	Ser	Pro	Tyr
		115				120						125			
Glu	Pro	Val	Thr	Ser	Arg	Leu	Ser	Asp	Ile	Phe	Arg	Leu	Ala	Ser	Ile
		130				135					140				



Phe	Ser	Gly	Thr	Gly	Ala	Asp	Pro	Val	Val	Ser	Ala	Lys	Ser	Asn	His	145	150	155	160
Cys	Leu	Asp	Ala	Ala	Lys	Ala	Cys	Asn	Leu	Asn	Asp	Asn	Cys	Lys	Lys	165	170	175	
Leu	Arg	Ser	Ser	Tyr	Ile	Ser	Ile	Cys	Asn	Arg	Glu	Ile	Ser	Pro	Thr	180	185	190	
Glu	Arg	Cys	Asn	Arg	Arg	Lys	Cys	His	Lys	Ala	Leu	Arg	Gln	Phe	Phe	195	200	205	
Asp	Arg	Val	Pro	Ser	Glu	Tyr	Thr	Tyr	Arg	Met	Leu	Phe	Cys	Ser	Cys	210	215	220	
Gln	Asp	Gln	Ala	Cys	Ala	Glu	Arg	Arg	Arg	Gln	Thr	Ile	Leu	Pro	Ser	225	230	235	240
Cys	Ser	Tyr	Glu	Asp	Lys	Glu	Lys	Pro	Asn	Cys	Leu	Asp	Leu	Arg	Gly	245	250	255	
Val	Cys	Arg	Thr	Asp	His	Leu	Cys	Arg	Ser	Arg	Leu	Ala	Asp	Phe	His	260	265	270	
Ala	Asn	Cys	Arg	Ala	Ser	Tyr	Gln	Thr	Val	Thr	Ser	Cys	Pro	Ala	Asp	275	280	285	
Asn	Tyr	Gln	Ala	Cys	Leu	Gly	Ser	Tyr	Ala	Gly	Met	Ile	Gly	Phe	Asp	290	295	300	
Met	Thr	Pro	Asn	Tyr	Val	Asp	Ser	Ser	Pro	Thr	Gly	Ile	Val	Val	Ser	305	310	315	320
Pro	Trp	Cys	Ser	Cys	Arg	Gly	Ser	Gly	Asn	Met	Glu	Glu	Glu	Cys	Glu	325	330	335	
Lys	Phe	Leu	Arg	Asp	Phe	Thr	Glu	Asn	Pro	Cys	Leu	Arg	Asn	Ala	Ile	340	345	350	
Gln	Ala	Phe	Gly	Asn	Gly	Thr	Asp	Val	Asn	Val	Ser	Pro	Lys	Gly	Pro	355	360	365	
Ser	Phe	Gln	Ala	Thr	Gln	Ala	Pro	Arg	Val	Glu	Lys	Thr	Pro	Ser	Leu	370	375	380	
Pro	Asp	Asp	Leu	Ser	Asp	Ser	Thr	Ser	Leu	Gly	Thr	Ser	Val	Ile	Thr	385	390	395	400
Thr	Cys	Thr	Ser	Val	Gln	Glu	Gln	Gly	Leu	Lys	Ala	Asn	Asn	Ser	Lys	405	410	415	
Glu	Leu	Ser	Met	Cys	Phe	Thr	Glu	Leu	Thr	Thr	Asn	Ile	Ile	Pro	Gly	420	425	430	
Ser	Asn	Lys	Val	Ile	Lys	Pro	Asn	Ser	Gly	Pro	Ser	Arg	Ala	Arg	Pro	435	440	445	
Ser	Ala	Ala	Leu	Thr	Val	Leu	Ser	Val	Leu	Met	Leu	Lys	Leu	Ala	Leu	450	455	460	

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

CGCGGCGCCC AGCGCAGGCA GAGCGCTGTC GCATCCCGGG CGTCCACCCG CCATGGGGCT

CTCCTGGAGC CCGCGACCTC CACTGCTGAT GATCCTGCTA CTGGTGCTGT CGTTGTGGCT

GCCACTTGGA GCAGGAAACT CCCTTGCCAC AGAGAACAGG TTTGTGAACA GCTGTACCCA

GGCCAGAAAG AAATGCGAGG CTAA TCC CGC TTG CAA GGC TGC CTA CCA GCA

Ser Arg Leu Gln Gly Cys Leu Pro Ala  
465 470

CCT GGG CTC CTG CAC CTC CAG TTA AGC AGG CCG CTG CCC TTA GAG GAG

Pro Gly Leu Leu His Leu Gln Leu Ser Arg Pro Leu Pro Leu Glu Glu  
475 480 485

TCT GCC ATG TCT GCA GAC TGC CTA GAG GCA GCA GAA CAA CTC AGG AAC

Ser Ala Met Ser Ala Asp Cys Leu Glu Ala Ala Glu Gln Leu Arg Asn  
490 495 500 505

AGC TCT CTG ATA GAC TGC AGG TGC CAT CGG CGC ATG AAG CAC CAA GCT

Ser Ser Leu Ile Asp Cys Arg Cys His Arg Arg Met Lys His Gln Ala  
510 515 520

ACC TGT CTG GAC ATT TAT TGG ACC GTT CAC CCT GCC CGA AGC CTT GGT

Thr Cys Leu Asp Ile Tyr Trp Thr Val His Pro Ala Arg Ser Leu Gly  
525 530 535

GAC TAC GAG TTG GAT GTC TCA CCC TAT GAA GAC ACA GTG ACC AGC AAA

Asp Tyr Glu Leu Asp Val Ser Pro Tyr Glu Asp Thr Val Thr Ser Lys  
540 545 550

CCC TGG AAA ATG AAT CTT AGC AAG TTG AAC ATG CTC AAA CCA GAC TCG

Pro Trp Lys Met Asn Leu Ser Lys Leu Asn Met Leu Lys Pro Asp Ser  
555 560 565

GAC CTC TGC CTC AAA TTT GCT ATG CTG TGT ACT CTT CAC GAC AAG TGT

Asp Leu Cys Leu Lys Phe Ala Met Leu Cys Thr Leu His Asp Lys Cys  
570 575 580 585

615 GAC CGC CTG CGC AAG GCC TAC GGG GAG GCA TGC TCA GGG ATC CGC TGC  
 Asp Arg Leu Arg Lys Ala Tyr Gly Glu Ala Cys Ser Gly Ile Arg Cys  
 590 595 600

663 CAG CGC CAC CTC TGC CTA GCC CAG CTG CGC TCC TTC TTT GAG AAG GCA  
 Gln Arg His Leu Cys Leu Ala Gln Leu Arg Ser Phe Phe Glu Lys Ala  
 605 610 615

711 GCA GAG TCC CAC GCT CAG GGT CTG CTG CTG TGT CCC TGT GCA CCA GAA  
 Ala Glu Ser His Ala Gln Gly Leu Leu Leu Cys Pro Cys Ala Pro Glu  
 620 625 630

759 GAT GCG GGC TGT GGG GAG CGG CGG CGT AAC ACC ATC GCC CCC AGT TGC  
 Asp Ala Gly Cys Gly Glu Arg Arg Arg Asn Thr Ile Ala Pro Ser Cys  
 635 640 645

807 GCC CTG CCT TCT GTA ACC CCC AAT TGC CTG GAT CTG CGG AGC TTC TGC  
 Ala Leu Pro Ser Val Thr Pro Asn Cys Leu Asp Leu Arg Ser Phe Cys  
 650 655 660 665

855 CGT GCG GAC CCT TTG TGC AGA TCA CGC CTG ATG GAC TTC CAG ACC CAC  
 Arg Ala Asp Pro Leu Cys Arg Ser Arg Leu Met Asp Phe Gln Thr His  
 670 675 680

903 TGT CAT CCT ATG GAC ATC CTT GGG ACT TGT GCA ACT GAG CAG TCC AGA  
 Cys His Pro Met Asp Ile Leu Gly Thr Cys Ala Thr Glu Gln Ser Arg  
 685 690 695

951 TGT CTG CGG GCA TAC CTG GGG CTG ATT GGG ACT GCC ATG ACC CCA AAC  
 Cys Leu Arg Ala Tyr Leu Gly Leu Ile Gly Thr Ala Met Thr Pro Asn  
 700 705 710

999 TTC ATC AGC AAG GTC AAC ACT ACT GTT GCC TTA AGC TGC ACC TGC CGA  
 Phe Ile Ser Lys Val Asn Thr Thr Val Ala Leu Ser Cys Thr Cys Arg  
 715 720 725

1047 GGC AGC GGC AAC CTA CAG GAC GAG TGT GAA CAG CTG GAA AGG TCC TTC  
 Gly Ser Gly Asn Leu Gln Asp Glu Cys Glu Gln Leu Glu Arg Ser Phe  
 730 735 740 745

1095 TCC CAG AAC CCC TGC CTC GTG GAG GCC ATT GCA GCT AAG ATG CGT TTC  
 Ser Gln Asn Pro Cys Leu Val Glu Ala Ile Ala Ala Lys Met Arg Phe  
 750 755 760

1143 CAC AGA CAG CTC TTC TCC CAG GAC TGG GCA GAC TCT ACT TTT TCA GTG  
 His Arg Gln Leu Phe Ser Gln Asp Trp Ala Asp Ser Thr Phe Ser Val  
 765 770 775

1191 GTG CAG CAG CAG AAC AGC AAC CCT GCT CTG AGA CTG CAG CCC AGG CTA  
 Val Gln Gln Gln Asn Ser Asn Pro Ala Leu Arg Leu Gln Pro Arg Leu  
 780 785 790

1239 CCC ATT CTT TCT TTC TCC ATC CTT CCC TTG ATT CTG CTG CAG ACC CTC  
 Pro Ile Leu Ser Phe Ser Ile Leu Pro Leu Ile Leu Leu Gln Thr Leu  
 795 800 805  
 1292 TGG TAGCTGGGCT TCCTCAGGGT CCTTTGTCCT CTCCACCACA CCCAGACTGA  
 Trp  
 810  
 1352 TTTGCAGCCT GTGGTGGGAG AGAACTCGCC AGCCTGTGGA AGAAGACGCA GCGTGCTACA  
 CAGCAACCCG GAACCAACCA GGCATTCCGC AGCACATCCC GTCTGCTCCA GAAGAGGTCT  
 1412  
 1472 TAGAAGTGAG GGCTGTGACC CTTCCGATCC TGAGCGGCTA GTTTTCAAAC CTCCCTTGCC  
 CCTGCTTCCT TCTGGCTCAG GCTGCTCCTC CTTAGGACTT TGTGGGTCCA GTTTTGCCTT  
 1532  
 1592 CTGTTCTGAT GGTGATTAGC GGCTCACCTC CAGCGCTTCT TCCTGTTTCC CAGGACCACC  
 CAGAGGCTAA GGAATCAGTC ATTCCCTGTT GCCTTCTCCA GGAAGGCAGG CTAAGGGTTC  
 1652  
 1712 TGAGGTGACT GAGAAAAATG TTTCTTTTGT GTGGAAGGCT GGTGCTCCAG CCTCCACGTC  
 CCTCTGAATG GAAGATAAAA ACCTGCTGGT GTCTTGACTG CTCTGCCAGG CAATCCTGAA  
 1772  
 1832 CATTTGGGCA TGAAGAGCTA AAGTCTTTGG GTCTTGTTTA ACTCCTATTA CTGTCCCCAA  
 1878 ATTCCCCTAG TCCCTTGGGT CATGATTAAA CATTTTGACT TAAAAA

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 346 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Ser	Arg	Leu	Gln	Gly	Cys	Leu	Pro	Ala	Pro	Gly	Leu	Leu	His	Leu	Gln
1				5					10					15	
Leu	Ser	Arg	Pro	Leu	Pro	Leu	Glu	Glu	Ser	Ala	Met	Ser	Ala	Asp	Cys
			20					25					30		
Leu	Glu	Ala	Ala	Glu	Gln	Leu	Arg	Asn	Ser	Ser	Leu	Ile	Asp	Cys	Arg
		35					40					45			
Cys	His	Arg	Arg	Met	Lys	His	Gln	Ala	Thr	Cys	Leu	Asp	Ile	Tyr	Trp
	50					55					60				
Thr	Val	His	Pro	Ala	Arg	Ser	Leu	Gly	Asp	Tyr	Glu	Leu	Asp	Val	Ser

65	70	75	80
Pro Tyr Glu Asp Thr Val Thr Ser Lys Pro Trp Lys Met Asn Leu Ser	85	90	95
Lys Leu Asn Met Leu Lys Pro Asp Ser Asp Leu Cys Leu Lys Phe Ala	100	105	110
Met Leu Cys Thr Leu His Asp Lys Cys Asp Arg Leu Arg Lys Ala Tyr	115	120	125
Gly Glu Ala Cys Ser Gly Ile Arg Cys Gln Arg His Leu Cys Leu Ala	130	135	140
Gln Leu Arg Ser Phe Phe Glu Lys Ala Ala Glu Ser His Ala Gln Gly	145	150	155
Leu Leu Leu Cys Pro Cys Ala Pro Glu Asp Ala Gly Cys Gly Glu Arg	165	170	175
Arg Arg Asn Thr Ile Ala Pro Ser Cys Ala Leu Pro Ser Val Thr Pro	180	185	190
Asn Cys Leu Asp Leu Arg Ser Phe Cys Arg Ala Asp Pro Leu Cys Arg	195	200	205
Ser Arg Leu Met Asp Phe Gln Thr His Cys His Pro Met Asp Ile Leu	210	215	220
Gly Thr Cys Ala Thr Glu Gln Ser Arg Cys Leu Arg Ala Tyr Leu Gly	225	230	235
Leu Ile Gly Thr Ala Met Thr Pro Asn Phe Ile Ser Lys Val Asn Thr	245	250	255
Thr Val Ala Leu Ser Cys Thr Cys Arg Gly Ser Gly Asn Leu Gln Asp	260	265	270
Glu Cys Glu Gln Leu Glu Arg Ser Phe Ser Gln Asn Pro Cys Leu Val	275	280	285
Glu Ala Ile Ala Ala Lys Met Arg Phe His Arg Gln Leu Phe Ser Gln	290	295	300
Asp Trp Ala Asp Ser Thr Phe Ser Val Val Gln Gln Gln Asn Ser Asn	305	310	315
Pro Ala Leu Arg Leu Gln Pro Arg Leu Pro Ile Leu Ser Phe Ser Ile	325	330	335
Leu Pro Leu Ile Leu Leu Gln Thr Leu Trp	340	345	

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1889 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 41..1231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

```
55 CGCAGGCAGA GCGCTGTCGC ATCCCGGGCG TCCACCCGCC ATG GGG CTC TCC TGG
Met Gly Leu Ser Trp
350

103 AGC CCG CGA CCT CCA CTG CTG ATG ATC CTG CTA CTG GTG CTG TCG TTG
Ser Pro Arg Pro Pro Leu Leu Met Ile Leu Leu Leu Val Leu Ser Leu
355 360 365

151 TGG CTG CCA CTT GGA GCA GGA AAC TCC CTT GCC ACA GAG AAC AGG TTT
Trp Leu Pro Leu Gly Ala Gly Asn Ser Leu Ala Thr Glu Asn Arg Phe
370 375 380

199 GTG AAC AGC TGT ACC CAG GCC AGA AAG AAA TGC GAG GCT AAT CCC GCT
Val Asn Ser Cys Thr Gln Ala Arg Lys Lys Cys Glu Ala Asn Pro Ala
385 390 395

247 TGC AAG GCT GCC TAC CAG CAC CTG GGC TCC TGC ACC TCC AGT TTA AGC
Cys Lys Ala Ala Tyr Gln His Leu Gly Ser Cys Thr Ser Ser Leu Ser
400 405 410 415

295 AGG CCG CTG CCC TTA GAG GAG TCT GCC ATG TCT GCA GAC TGC CTA GAG
Arg Pro Leu Pro Leu Glu Glu Ser Ala Met Ser Ala Asp Cys Leu Glu
420 425 430

343 GCA GCA GAA CAA CTC AGG AAC AGC TCT CTG ATA GAC TGC AGG TGC CAT
Ala Ala Glu Gln Leu Arg Asn Ser Ser Leu Ile Asp Cys Arg Cys His
435 440 445

391 CGG CGC ATG AAG CAC CAA GCT ACC TGT CTG GAC ATT TAT TGG ACC GTT
Arg Arg Met Lys His Gln Ala Thr Cys Leu Asp Ile Tyr Trp Thr Val
450 455 460

439 CAC CCT GCC CGA AGC CTT GGT GAC TAC GAG TTG GAT GTC TCA CCC TAT
His Pro Ala Arg Ser Leu Gly Asp Tyr Glu Leu Asp Val Ser Pro Tyr
465 470 475

487 GAA GAC ACA GTG ACC AGC AAA CCC TGG AAA ATG AAT CTT AGC AAG TTG
Glu Asp Thr Val Thr Ser Lys Pro Trp Lys Met Asn Leu Ser Lys Leu
480 485 490 495

535 AAC ATG CTC AAA CCA GAC TCG GAC CTC TGC CTC AAA TTT GCT ATG CTG
Asn Met Leu Lys Pro Asp Ser Asp Leu Cys Leu Lys Phe Ala Met Leu
500 505 510

583 TGT ACT CTT CAC GAC AAG TGT GAC CGC CTG CGC AAG GCC TAC GGG GAG
Cys Thr Leu His Asp Lys Cys Asp Arg Leu Arg Lys Ala Tyr Gly Glu
515 520 525
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631 GCA TGC TCA GGG ATC CGC TGC CAG CGC CAC CTC TGC CTA GCC CAG CTG  
 Ala Cys Ser Gly Ile Arg Cys Gln Arg His Leu Cys Leu Ala Gln Leu  
 530 535 540

679 CGC TCC TTC TTT GAG AAG GCA GCA GAG TCC CAC GCT CAG GGT CTG CTG  
 Arg Ser Phe Phe Glu Lys Ala Ala Glu Ser His Ala Gln Gly Leu Leu  
 545 550 555

727 CTG TGT CCC TGT GCA CCA GAA GAT GCG GGC TGT GGG GAG CGG CGG CGT  
 Leu Cys Pro Cys Ala Pro Glu Asp Ala Gly Cys Gly Glu Arg Arg Arg  
 560 565 570 575

775 AAC ACC ATC GCC CCC AGT TGC GCC CTG CCT TCT GTA ACC CCC AAT TGC  
 Asn Thr Ile Ala Pro Ser Cys Ala Leu Pro Ser Val Thr Pro Asn Cys  
 580 585 590

823 CTG GAT CTG CGG AGC TTC TGC CGT GCG GAC CCT TTG TGC AGA TCA CGC  
 Leu Asp Leu Arg Ser Phe Cys Arg Ala Asp Pro Leu Cys Arg Ser Arg  
 595 600 605

871 CTG ATG GAC TTC CAG ACC CAC TGT CAT CCT ATG GAC ATC CTT GGG ACT  
 Leu Met Asp Phe Gln Thr His Cys His Pro Met Asp Ile Leu Gly Thr  
 610 615 620

919 TGT GCA ACT GAG CAG TCC AGA TGT CTG CGG GCA TAC CTG GGG CTG ATT  
 Cys Ala Thr Glu Gln Ser Arg Cys Leu Arg Ala Tyr Leu Gly Leu Ile  
 625 630 635

967 GGG ACT GCC ATG ACC CCA AAC TTC ATC AGC AAG GTC AAC ACT ACT GTT  
 Gly Thr Ala Met Thr Pro Asn Phe Ile Ser Lys Val Asn Thr Thr Val  
 640 645 650 655

1015 GCC TTA AGC TGC ACC TGC CGA GGC AGC GGC AAC CTA CAG GAC GAG TGT  
 Ala Leu Ser Cys Thr Cys Arg Gly Ser Gly Asn Leu Gln Asp Glu Cys  
 660 665 670

1063 GAA CAG CTG GAA AGG TCC TTC TCC CAG AAC CCC TGC CTC GTG GAG GCC  
 Glu Gln Leu Glu Arg Ser Phe Ser Gln Asn Pro Cys Leu Val Glu Ala  
 675 680 685

1111 ATT GCA GCT AAG ATG CGT TTC CAC AGA CAG CTC TTC TCC CAG GAC TGG  
 Ile Ala Ala Lys Met Arg Phe His Arg Gln Leu Phe Ser Gln Asp Trp  
 690 695 700

1159 GCA GAC TCT ACT TTT TCA GTG GTG CAG CAG CAG AAC AGC AAC CCT GCT  
 Ala Asp Ser Thr Phe Ser Val Val Gln Gln Gln Asn Ser Asn Pro Ala  
 705 710 715

1207 CTG AGA CTG CAG CCC AGG CTA CCC ATT CTT TCT TTC TCC ATC CTT CCC  
 Leu Arg Leu Gln Pro Arg Leu Pro Ile Leu Ser Phe Ser Ile Leu Pro  
 720 725 730 735

1261 TTG ATT CTG CTG CAG ACC CTC TGG TAGCTGGGCT TCCTCAGGGT CCTTTGTCCT  
 Leu Ile Leu Leu Gln Thr Leu Trp  
 740  
 1321 CTCACACCACA CCCAGACTGA TTTGCAGCCT GTGGTGGGAG AGAACTCGCC AGCCTGTGGA  
 1381 AGAAGACGCA GCGTGCTACA CAGCAACCCG GAACCAACCA GGCATTCCGC AGCACATCCC  
 1441 GTCTGCTCCA GAAGAGGTCT TAGAAGTGAG GGCTGTGACC CTTCCGATCC TGAGCGGCTA  
 1501 GTTTTCAAAC CTCCCTTGCC CCTGCTTCCT TCTGGCTCAG GCTGCTCCTC CTTAGGACTT  
 1561 TGTGGGTCCA GTTTTCCTT CTGTTCTGAT GGTGATTAGC GGCTCACCTC CAGCGCTTCT  
 1621 TCCTGTTTCC CAGGACCACC CAGAGGCTAA GGAATCAGTC ATTCCCTGTT GCCTTCTCCA  
 1681 GGAAGGCAGG CTAAGGGTTC TGAGGTGACT GAGAAAAATG TTTCCTTTGT GTGGAAGGCT  
 1741 GGTGCTCCAG CCTCCACGTC CCTCTGAATG GAAGATAAAA ACCTGCTGGT GTCTTGACTG  
 1801 CTCTGCCAGG CAATCCTGAA CATTTGGGCA TGAAGAGCTA AAGTCTTTGG GTCTTGTTTA  
 1861 ACTCTATTA CTGTCCCCAA ATTCCCCTAG TCCCTGGGT CATGATTAAA CATTTTGACT  
 1889 TAAAAAAAAA AAAAAAAAAA AAAAAAAA

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 397 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met	Gly	Leu	Ser	Trp	Ser	Pro	Arg	Pro	Pro	Leu	Leu	Met	Ile	Leu	Leu
1				5					10					15	
Leu	Val	Leu	Ser	Leu	Trp	Leu	Pro	Leu	Gly	Ala	Gly	Asn	Ser	Leu	Ala
			20					25					30		
Thr	Glu	Asn	Arg	Phe	Val	Asn	Ser	Cys	Thr	Gln	Ala	Arg	Lys	Lys	Cys
		35					40					45			
Glu	Ala	Asn	Pro	Ala	Cys	Lys	Ala	Ala	Tyr	Gln	His	Leu	Gly	Ser	Cys
	50					55				60					
Thr	Ser	Ser	Leu	Ser	Arg	Pro	Leu	Pro	Leu	Glu	Glu	Ser	Ala	Met	Ser
65					70					75				80	





46	C	GGC	TAC	TGT	GAA	ACA	CCT	CAA	CTC	AGG	AAC	AGC	TCT	CTG	ATA	GGC	
	Gly	Tyr	Cys	Glu	Thr	Pro	Gln	Leu	Arg	Asn	Ser	Ser	Leu	Ile	Gly		
			400					405						410			
94	TGC	ATG	TGC	CAC	CGG	CGC	ATG	AAG	AAC	CAG	GTT	GCC	TGC	TTG	GAC	ATC	
	Cys	Met	Cys	His	Arg	Arg	Met	Lys	Asn	Gln	Val	Ala	Cys	Leu	Asp	Ile	
			415					420					425				
142	TAT	TGG	ACC	GTT	CAC	CGT	GCC	CGC	AGC	CTT	GGT	AAC	TAT	GAG	CTG	GAT	
	Tyr	Trp	Thr	Val	His	Arg	Ala	Arg	Ser	Leu	Gly	Asn	Tyr	Glu	Leu	Asp	
		430					435					440					
190	GTC	TCC	CCC	TAT	GAA	GAC	ACA	GTG	ACC	AGC	AAA	CCC	TGG	AAA	ATG	AAT	
	Val	Ser	Pro	Tyr	Glu	Asp	Thr	Val	Thr	Ser	Lys	Pro	Trp	Lys	Met	Asn	
		445				450					455					460	
238	CTC	AGC	AAA	CTG	AAC	ATG	CTC	AAA	CCA	GAC	TCA	GAC	CTC	TGC	CTC	AAG	
	Leu	Ser	Lys	Leu	Asn	Met	Leu	Lys	Pro	Asp	Ser	Asp	Leu	Cys	Leu	Lys	
					465					470					475		
286	TTT	GCC	ATG	CTG	TGT	ACT	CTC	AAT	GAC	AAG	TGT	GAC	CGG	CTG	CGC	AAG	
	Phe	Ala	Met	Leu	Cys	Thr	Leu	Asn	Asp	Lys	Cys	Asp	Arg	Leu	Arg	Lys	
				480					485					490			
334	GCC	TAC	GGG	GAG	GCG	TGC	TCC	GGG	CCC	CAC	TGC	CAG	CGC	CAC	GTC	TGC	
	Ala	Tyr	Gly	Glu	Ala	Cys	Ser	Gly	Pro	His	Cys	Gln	Arg	His	Val	Cys	
			495					500					505				
382	CTC	AGG	CAG	CTG	CTC	ACT	TTC	TTC	GAG	AAG	GCC	GCC	GAG	CCC	CAC	GCG	
	Leu	Arg	Gln	Leu	Leu	Thr	Phe	Phe	Glu	Lys	Ala	Ala	Glu	Pro	His	Ala	
		510					515					520					
430	CAG	GGC	CTG	CTA	CTG	TGC	CCA	TGT	GCC	CCC	AAC	GAC	CGG	GGC	TGC	GGG	
	Gln	Gly	Leu	Leu	Leu	Cys	Pro	Cys	Ala	Pro	Asn	Asp	Arg	Gly	Cys	Gly	
		525				530					535					540	
478	GAG	CGC	CGG	CGC	AAC	ACC	ATC	GCC	CCC	AAC	TGC	GCG	CTG	CCG	CCT	GTG	
	Glu	Arg	Arg	Arg	Asn	Thr	Ile	Ala	Pro	Asn	Cys	Ala	Leu	Pro	Pro	Val	
					545					550					555		

526 GCC CCC AAC TGC CTG GAG CTG CGG CGC CTC TGC TTC TCC GAC CCG CTT  
 Ala Pro Asn Cys Leu Glu Leu Arg Arg Leu Cys Phe Ser Asp Pro Leu  
 560 565 570

574 TGC AGA TCA CGC CTG GTG GAT TTC CAG ACC CAC TGC CAT CCC ATG GAC  
 Cys Arg Ser Arg Leu Val Asp Phe Gln Thr His Cys His Pro Met Asp  
 575 580 585

622 ATC CTA GGA ACT TGT GCA ACA GAG CAG TCC AGA TGT CTA CGA GCA TAC  
 Ile Leu Gly Thr Cys Ala Thr Glu Gln Ser Arg Cys Leu Arg Ala Tyr  
 590 595 600

670 CTG GGG CTG ATT GGG ACT GCC ATG ACC CCC AAC TTT GTC AGC AAT GTC  
 Leu Gly Leu Ile Gly Thr Ala Met Thr Pro Asn Phe Val Ser Asn Val  
 605 610 615 620

718 AAC ACC AGT GTT GCC TTA AGC TGC ACC TGC CGA GGC AGT GGC AAC CTG  
 Asn Thr Ser Val Ala Leu Ser Cys Thr Cys Arg Gly Ser Gly Asn Leu  
 625 630 635

766 CAG GAG GAG TGT GAA ATG CTG GAA GGG TTC TTC TCC CAC AAC CCC TGC  
 Gln Glu Glu Cys Glu Met Leu Glu Gly Phe Phe Ser His Asn Pro Cys  
 640 645 650

814 CTC ACG GAG GCC ATT GCA GCT AAG ATG CGT TTT CAC AGC CAA CTC TTC  
 Leu Thr Glu Ala Ile Ala Ala Lys Met Arg Phe His Ser Gln Leu Phe  
 655 660 665

862 TCC CAG GAC TGG CCA CAC CCT ACC TTT GCT GTG ATG GCA CAC CAG AAT  
 Ser Gln Asp Trp Pro His Pro Thr Phe Ala Val Met Ala His Gln Asn  
 670 675 680

910 GAA AAC CCT GCT GTG AGG CCA CAG CCC TGG GTG CCC TCT CTT TTC TCC  
 Glu Asn Pro Ala Val Arg Pro Gln Pro Trp Val Pro Ser Leu Phe Ser  
 685 690 695 700

956 TGC ACG CTT CCC TTG ATT CTG CTC CTG AGC CTA TGG TAGCTGGACT  
 Cys Thr Leu Pro Leu Ile Leu Leu Leu Ser Leu Trp  
 705 710

1016 TCCCCAGGGC CCTCTTCCCC TCCACCACAC CCAGGTGGAC TTGCAGCCCA CAAGGGGTGA

1076 GGAAAGGACA GCAGCAGGAA GGAGGTGCAG TGCGCAGATG AGGGCACAGG AGAAGCTAAG

1136 GGTTATGACC TCCAGATCCT TACTGGTCCA GTCCTCATTC CCTCCACCCC ATCTCCACTT

1196 CTGATTCATG CTGCCCCCTCC TTGGTGGCCA CAATTTAGCC ATGTCATCTG GTGCCTGTGG

1256 GCCTTGCTTT ATTCCTATTA TTGTCCTAAA GTCTCTCTGG GCTCTTGGAT CATGATTAAA

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 315 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Gly	Tyr	Cys	Glu	Thr	Pro	Gln	Leu	Arg	Asn	Ser	Ser	Leu	Ile	Gly	Cys	1	5	10	15
Met	Cys	His	Arg	Arg	Met	Lys	Asn	Gln	Val	Ala	Cys	Leu	Asp	Ile	Tyr	20	25	30	
Trp	Thr	Val	His	Arg	Ala	Arg	Ser	Leu	Gly	Asn	Tyr	Glu	Leu	Asp	Val	35	40	45	
Ser	Pro	Tyr	Glu	Asp	Thr	Val	Thr	Ser	Lys	Pro	Trp	Lys	Met	Asn	Leu	50	55	60	
Ser	Lys	Leu	Asn	Met	Leu	Lys	Pro	Asp	Ser	Asp	Leu	Cys	Leu	Lys	Phe	65	70	75	80
Ala	Met	Leu	Cys	Thr	Leu	Asn	Asp	Lys	Cys	Asp	Arg	Leu	Arg	Lys	Ala	85	90	95	
Tyr	Gly	Glu	Ala	Cys	Ser	Gly	Pro	His	Cys	Gln	Arg	His	Val	Cys	Leu	100	105	110	
Arg	Gln	Leu	Leu	Thr	Phe	Phe	Glu	Lys	Ala	Ala	Glu	Pro	His	Ala	Gln	115	120	125	
Gly	Leu	Leu	Leu	Cys	Pro	Cys	Ala	Pro	Asn	Asp	Arg	Gly	Cys	Gly	Glu	130	135	140	
Arg	Arg	Arg	Asn	Thr	Ile	Ala	Pro	Asn	Cys	Ala	Leu	Pro	Pro	Val	Ala	145	150	155	160
Pro	Asn	Cys	Leu	Glu	Leu	Arg	Arg	Leu	Cys	Phe	Ser	Asp	Pro	Leu	Cys	165	170	175	
Arg	Ser	Arg	Leu	Val	Asp	Phe	Gln	Thr	His	Cys	His	Pro	Met	Asp	Ile	180	185	190	
Leu	Gly	Thr	Cys	Ala	Thr	Glu	Gln	Ser	Arg	Cys	Leu	Arg	Ala	Tyr	Leu	195	200	205	
Gly	Leu	Ile	Gly	Thr	Ala	Met	Thr	Pro	Asn	Phe	Val	Ser	Asn	Val	Asn	210	215	220	
Thr	Ser	Val	Ala	Leu	Ser	Cys	Thr	Cys	Arg	Gly	Ser	Gly	Asn	Leu	Gln	225	230	235	240
Glu	Glu	Cys	Glu	Met	Leu	Glu	Gly	Phe	Phe	Ser	His	Asn	Pro	Cys	Leu	245	250	255	
Thr	Glu	Ala	Ile	Ala	Ala	Lys	Met	Arg	Phe	His	Ser	Gln	Leu	Phe	Ser	260	265	270	

Gln Asp Trp Pro His Pro Thr Phe Ala Val Met Ala His Gln Asn Glu  
 275 280 285

Asn Pro Ala Val Arg Pro Gln Pro Trp Val Pro Ser Leu Phe Ser Cys  
 290 295 300

Thr Leu Pro Leu Ile Leu Leu Leu Ser Leu Trp  
 305 310 315

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1699 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 175..1374

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

60 TGTGGACGCG CGCTTCGGAG TTGGAGGGCG GCGCCAGGA CCCTGGTGGG AGAGTGTGTG

120 CGTCGCGCTG GAGGGCGGGA GGCGGGGCG GGAGGTGCCG GTCGAGGGAG CCCCCTCTC

177 AGAGCTCCAG GGGAGGAGCG AGGGGAGCGC GGAGCCCGGC GCCTACAGCT CGCC ATG  
 Met

225 GTG CGC CCC CTG AAC CCG CGA CCG CTG CCG CCC GTA GTC CTG ATG TTG  
 Val Arg Pro Leu Asn Pro Arg Pro Leu Pro Pro Val Val Leu Met Leu  
 320 325 330

273 CTG CTG CTG CTG CCG CCG TCG CCG CTG CCT CTC GCA GCC GGA GAC CCC  
 Leu Leu Leu Leu Pro Pro Ser Pro Leu Pro Leu Ala Ala Gly Asp Pro  
 335 340 345

321 CTT CCC ACA GAA AGC CGA CTC ATG AAC AGC TGT CTC CAG GCC AGG AGG  
 Leu Pro Thr Glu Ser Arg Leu Met Asn Ser Cys Leu Gln Ala Arg Arg  
 350 355 360

369 AAG TGC CAG GCT GAT CCC ACC TGC AGT GCT GCC TAC CAC CAC CTG GAT  
 Lys Cys Gln Ala Asp Pro Thr Cys Ser Ala Ala Tyr His His Leu Asp  
 365 370 375 380

417 TCC TGC ACC TCT AGC ATA AGC ACC CCA CTG CCC TCA GAG GAG CCT TCG  
 Ser Cys Thr Ser Ser Ile Ser Thr Pro Leu Pro Ser Glu Glu Pro Ser  
 385 390 395

465 GTC CCT GCT GAC TGC CTG GAG GCA GCA CAG CAA CTC AGG AAC AGC TCT  
 Val Pro Ala Asp Cys Leu Glu Ala Ala Gln Gln Leu Arg Asn Ser Ser  
 400 405 410

513 CTG ATA GGC TGC ATG TGC CAC CGG CGC ATG AAG AAC CAG GTT GCC TGC  
 Leu Ile Gly Cys Met Cys His Arg Arg Met Lys Asn Gln Val Ala Cys  
 415 420 425

561 TTG GAC ATC TAT TGG ACC GTT CAC CGT GCC CGC AGC CTT GGT AAC TAT  
 Leu Asp Ile Tyr Trp Thr Val His Arg Ala Arg Ser Leu Gly Asn Tyr  
 430 435 440

609 GAG CTG GAT GTC TCC CCC TAT GAA GAC ACA GTG ACC AGC AAA CCC TGG  
 Glu Leu Asp Val Ser Pro Tyr Glu Asp Thr Val Thr Ser Lys Pro Trp  
 445 450 455 460

657 AAA ATG AAT CTC AGC AAA CTG AAC ATG CTC AAA CCA GAC TCA GAC CTC  
 Lys Met Asn Leu Ser Lys Leu Asn Met Leu Lys Pro Asp Ser Asp Leu  
 465 470 475

705 TGC CTC AAG TTT GCC ATG CTG TGT ACT CTC AAT GAC AAG TGT GAC CGG  
 Cys Leu Lys Phe Ala Met Leu Cys Thr Leu Asn Asp Lys Cys Asp Arg  
 480 485 490

753 CTG CGC AAG GCC TAC GGG GAG GCG TGC TCC GGG CCC CAC TGC CAG CGC  
 Leu Arg Lys Ala Tyr Gly Glu Ala Cys Ser Gly Pro His Cys Gln Arg  
 495 500 505

801 CAC GTC TGC CTC AGG CAG CTG CTC ACT TTC TTC GAG AAG GCC GCC GAG  
 His Val Cys Leu Arg Gln Leu Leu Thr Phe Phe Glu Lys Ala Ala Glu  
 510 515 520

849 CCC CAC GCG CAG GGC CTG CTA CTG TGC CCA TGT GCC CCC AAC GAC CGG  
 Pro His Ala Gln Gly Leu Leu Leu Cys Pro Cys Ala Pro Asn Asp Arg  
 525 530 535 540

897 GGC TGC GGG GAG CGC CGG CGC AAC ACC ATC GCC CCC AAC TGC GCG CTG  
 Gly Cys Gly Glu Arg Arg Arg Asn Thr Ile Ala Pro Asn Cys Ala Leu  
 545 550 555

945 CCG CCT GTG GCC CCC AAC TGC CTG GAG CTG CGG CGC CTC TGC TTC TCC  
 Pro Pro Val Ala Pro Asn Cys Leu Glu Leu Arg Arg Leu Cys Phe Ser  
 560 565 570

993 GAC CCG CTT TGC AGA TCA CGC CTG GTG GAT TTC CAG ACC CAC TGC CAT  
 Asp Pro Leu Cys Arg Ser Arg Leu Val Asp Phe Gln Thr His Cys His  
 575 580 585

1041 CCC ATG GAC ATC CTA GGA ACT TGT GCA ACA GAG CAG TCC AGA TGT CTA  
 Pro Met Asp Ile Leu Gly Thr Cys Ala Thr Glu Gln Ser Arg Cys Leu  
 590 595 600

1089 CGA GCA TAC CTG GGG CTG ATT GGG ACT GCC ATG ACC CCC AAC TTT GTC  
 Arg Ala Tyr Leu Gly Leu Ile Gly Thr Ala Met Thr Pro Asn Phe Val  
 605 610 615 620  
 1137 AGC AAT GTC AAC ACC AGT GTT GCC TTA AGC TGC ACC TGC CGA GGC AGT  
 Ser Asn Val Asn Thr Ser Val Ala Leu Ser Cys Thr Cys Arg Gly Ser  
 625 630 635  
 1185 GGC AAC CTG CAG GAG GAG TGT GAA ATG CTG GAA GGG TTC TTC TCC CAC  
 Gly Asn Leu Gln Glu Glu Cys Glu Met Leu Glu Gly Phe Phe Ser His  
 640 645 650  
 1233 AAC CCC TGC CTC ACG GAG GCC ATT GCA GCT AAG ATG CGT TTT CAC AGC  
 Asn Pro Cys Leu Thr Glu Ala Ile Ala Ala Lys Met Arg Phe His Ser  
 655 660 665  
 1281 CAA CTC TTC TCC CAG GAC TGG CCA CAC CCT ACC TTT GCT GTG ATG GCA  
 Gln Leu Phe Ser Gln Asp Trp Pro His Pro Thr Phe Ala Val Met Ala  
 670 675 680  
 1329 CAC CAG AAT GAA AAC CCT GCT GTG AGG CCA CAG CCC TGG GTG CCC TCT  
 His Gln Asn Glu Asn Pro Ala Val Arg Pro Gln Pro Trp Val Pro Ser  
 685 690 695 700  
 1374 CTT TTC TCC TGC ACG CTT CCC TTG ATT CTG CTC CTG AGC CTA TGG  
 Leu Phe Ser Cys Thr Leu Pro Leu Ile Leu Leu Leu Ser Leu Trp  
 705 710 715  
 1434 TAGCTGGACT TCCCCAGGGC CCTCTTCCCC TCCACCACAC CCAGGTGGAC TTGCAGCCCA  
 1494 CAAGGGGTGA GGAAAGGACA GCAGCAGGAA GGAGGTGCAG TGCGCAGATG AGGGCACAGG  
 1554 AGAAGCTAAG GGTATGACC TCCAGATCCT TACTGGTCCA GTCCTCATTC CCTCCACCCC  
 1614 ATCTCCACTT CTGATTCATG CTGCCCCCTCC TTGGTGGCCA CAATTTAGCC ATGTCATCTG  
 1674 GTGCCTGTGG GCCTTGCTTT ATTCCTATTA TTGTCCTAAA GTCTCTCTGG GCTCTTGGAT  
 1699 CATGATTAAA CCTTTGACTT AAAAA

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met Val Arg Pro Leu Asn Pro Arg Pro Leu Pro Pro Val Val Leu Met  
 1 5 10 15  
 Leu Leu Leu Leu Leu Pro Pro Ser Pro Leu Pro Leu Ala Ala Gly Asp  
 20 25 30  
 Pro Leu Pro Thr Glu Ser Arg Leu Met Asn Ser Cys Leu Gln Ala Arg  
 35 40 45  
 Arg Lys Cys Gln Ala Asp Pro Thr Cys Ser Ala Ala Tyr His His Leu  
 50 55 60  
 Asp Ser Cys Thr Ser Ser Ile Ser Thr Pro Leu Pro Ser Glu Glu Pro  
 65 70 75 80  
 Ser Val Pro Ala Asp Cys Leu Glu Ala Ala Gln Gln Leu Arg Asn Ser  
 85 90 95  
 Ser Leu Ile Gly Cys Met Cys His Arg Arg Met Lys Asn Gln Val Ala  
 100 105 110  
 Cys Leu Asp Ile Tyr Trp Thr Val His Arg Ala Arg Ser Leu Gly Asn  
 115 120 125  
 Tyr Glu Leu Asp Val Ser Pro Tyr Glu Asp Thr Val Thr Ser Lys Pro  
 130 135 140  
 Trp Lys Met Asn Leu Ser Lys Leu Asn Met Leu Lys Pro Asp Ser Asp  
 145 150 155 160  
 Leu Cys Leu Lys Phe Ala Met Leu Cys Thr Leu Asn Asp Lys Cys Asp  
 165 170 175  
 Arg Leu Arg Lys Ala Tyr Gly Glu Ala Cys Ser Gly Pro His Cys Gln  
 180 185 190  
 Arg His Val Cys Leu Arg Gln Leu Leu Thr Phe Phe Glu Lys Ala Ala  
 195 200 205  
 Glu Pro His Ala Gln Gly Leu Leu Leu Cys Pro Cys Ala Pro Asn Asp  
 210 215 220  
 Arg Gly Cys Gly Glu Arg Arg Arg Asn Thr Ile Ala Pro Asn Cys Ala  
 225 230 235 240  
 Leu Pro Pro Val Ala Pro Asn Cys Leu Glu Leu Arg Arg Leu Cys Phe  
 245 250 255  
 Ser Asp Pro Leu Cys Arg Ser Arg Leu Val Asp Phe Gln Thr His Cys  
 260 265 270  
 His Pro Met Asp Ile Leu Gly Thr Cys Ala Thr Glu Gln Ser Arg Cys  
 275 280 285  
 Leu Arg Ala Tyr Leu Gly Leu Ile Gly Thr Ala Met Thr Pro Asn Phe  
 290 295 300  
 Val Ser Asn Val Asn Thr Ser Val Ala Leu Ser Cys Thr Cys Arg Gly  
 305 310 315 320  
 Ser Gly Asn Leu Gln Glu Glu Cys Glu Met Leu Glu Gly Phe Phe Ser  
 325 330 335  
 His Asn Pro Cys Leu Thr Glu Ala Ile Ala Ala Lys Met Arg Phe His  
 340 345 350



Ser Gln Leu Phe Ser Gln Asp Trp Pro His Pro Thr Phe Ala Val Met  
355 360 365

Ala His Gln Asn Glu Asn Pro Ala Val Arg Pro Gln Pro Trp Val Pro  
370 375 380

Ser Leu Phe Ser Cys Thr Leu Pro Leu Ile Leu Leu Leu Ser Leu Trp  
385 390 395 400